Page 1

0

IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences

Results file Seq2-Peps.res made by tport on Fri 28 Feb 103 11:22:23-PST

Number of sequences searched: Number of scores above cutoff:

Results of the initial comparison of US-09-978-385-2 (1-805) with: File : US09978385.pep

Z D Z U Z

50-

m 0

10-

SECNECNES

SCORE STDEV

89

358 | 447

537

626

1 1 1

0---

Gap penalty
Gap size penalty

5.00

Randomization group

SEARCH STATISTICS

Number of residues: Number of sequences searched: Number of scores above cutoff:

The scores below are sorted by initial score. Significance is calculated based on initial score.

100% identical sequence to the query sequence was found:

Init. Opt. Length Score Score Sig. Frame

Sequence Name

Times: Scores:

00:00:00.00

Total Elapsed 00:00:00:00.00

Standard Deviation 383.50

2431

Similarity matrix Threshold level of sim. Mismatch penalty

PAM-150

K-tuple Window Joining penalty

500

PARAMETERS

Query sequence being compared: US-09-978-385-2 (1-805)

1

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The list of other best scores is:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Name
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                    Residue Identity =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. US-09-978-385-2 Sequence 2, Application US
                                                                                                                                                                                                                                                                                                                                                                                                                 2. US-09-978-385-6 Sequence 🚣 Application US 3. US-09-978-385-9 Sequence 🚣 Application US
                                                                                                                                                                                                                                                                                                                                                                                         US-09-978-385-2 (1-805)
US-09-978-385-2 Sequence 2, Application US/09978385
                                                                                                                                                                                                                                                                                                                            MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNWNNAGDKWSAF
                                                                                                                                                                                                                                                                                    KNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDMSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
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100%
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                             630
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                                                                                                              500
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Residue Identity =
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                                                              ETEINFLKQALTIVGTLPETYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLE
                                                                                               ETEINELLKOALTIVGTLPETYMLEKWRWMVFRGEIPKEOWMKKWWEMKREIVGVVEPLPHDETYCDPASLF
                                                                                                                                                                                            YNRNÓLIEDVERTFAREIKPLYEHLHAYVRRKLMDTYPSYISPTGCLPAHLLGDMWGRFWTNLYPLTVPFAQK
220 230 240 250 260 270 280
                                                                                                                                                                                                          YSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGGLPAHLLGDMWGRFWTNLYSLTVPFGOK
                                                                                                                                                                                                                                                 US-09-978-385-6 Sequence 6, Application US/09978385
                                                                                                                                                                                                                                                                                                                                                       MSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAF
                                                                                                                                                                                                                                                                                                                                               MSSSSWLLLSLVAVTTAQSLTEENAKTFLNNFNQEAEDLSYQSSLASWNYNTNTTEENAQKNSEAAAKWSAF
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Residue Identity =
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US-09-978-385-9 Sequence 9, Application US/09978385
PNIDVTDAMMNOGWDAERIFQEAEKFFVSVGLPHMTQGFWANSMITEPADGRKVVCHPTAWDLGHGDFRIKM
                                                                                                                                                                                                                          PNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLPNWTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM
                                                                                                                                                                                                                                                                                                            vnrnoliedvertéaetkelyehlhayvrrkimdtyesvisetgéleahligdnygrewinlyeltvefaok
                                                                                                                                                                                                                                                                                                                              YSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLIGDMWGRFWTNLYSLTVPFGOK
                                                                                                                                                                                                                                                                                                                                                                                                               LKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQECLLLYEEQSKTAQSFSLQEIQTPIIKRQLQALQQSGSSALSADKNKQLNTILNTMSTIYSTGKVCNPRNPQECLLLYEEQSKTAQSFSLQEIQTPIIKRQLQALQQSGSSALSADKNKQLNTILNTMSTIYSTGKVCNPRNPQECLLLYEEQSKTAQSFSLQEIQTPIIKRQLQALQQSGSSALSADKNKQLNTILNTMSTIYSTGKVCNPRNPQECLLLYEEQSKTAQSFSLQEIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSSSSWILLSLVAVTTAQSLTEENAKTFLNNFNQEAEDLSYQSSLASWNYNTNITEENAQKMSEAAAKWSAF
X 10 50 60 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSSSSWLLLSIVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YAMRQYFLKVKNQMILEGEEDVRVANLKPRISENFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNMNVRDLLNYFEPLETWLKDONKNSFVGWSTDWSDYADOSIKVRISLKSALGDKAYEWNDNEWYLFRSSVARIMDVKPLLNYFEPLETWLKDONKNSFVGWSTDWSDYADOSIKVRISLKSALGDKAYEWNDNEWYLFRSSVARIMDVKPLLNYFGQPLFDWLKEQNRNSFVGWNTEWSPYADOSIKVRISLKSALGANAYEWTNNEWFLFRSSVARIMDVKPLLNYFQPLFDWLKEQNRNSFVGWNTEWSPYADOSIKVRISLKSALGANAYEWTNNEWFLFRSSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAMRKYESTIKNOTVPELEEDVRVSDLKBRVSEYFFVTSPONVSDVIPRSEVEDAIRMSRGRINDVFGLNDN
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81% Marches = 659
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PGFQNTDDVQTSF	730 740 750 770 780 790 SLEFLGIQPTLGPPNOPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDKKKNKARSGENPYASIDISKGENN	650 650 670 720 720 720 720 720 720 720 720 720 7	580 590 600 600 520 620 620 820 KNMNYPLLINYFEPLETWIKDONKNSFYGWSTDWSFYADQSKYRISIKSALGDKAYEWNINEMYLFRSSYA († 11 1 1 1 1 1 1 1 1 1	510 520 530 540 550 550 570 HVSNDYSFIRYYTRTLYQEQEQEALCQAAKHEGELHKCDISNSTEAGOKLENMERLGKSEDWTLALENIVVGA	440
X X X X X X X X X X X X X X X X X X X	740 GPPNQPPVSIV EPPYQPPVTIV 740	0 670 NQMILFGEEDVI : NQTVPFLEEDVI	590 E	520 TRTLYQEQEC [TRTIYQEQEC 520	450
	750 VLITEGVVMGV VLITEGVVMAI 750	680 /RVANLKPRISI : : /RVSDLKPRVSI 680	600 6 QNKNSFVGWST : QNRNSFVGWNT 600 6	530 EALCQAAKHE EALCQAAKYN 530	460
	760 TIVVGIVILIF : : ;VVVGIIILIV 760	690 	610 6 STDWSPYADQSI : WTEWSPYADQSI 610 6	540 GPLHKCDISN: - - - GSLHKCDISN: 540	470
	770 TGIRDRKKN : TGIKGRKKN 770	700 VSDIIPRTEVI : VSDVIPRSEVI 700	620 630 	550 STEAGQKLFNN STEAGQKLLKN	480
	780 KARSGENPYAS : ETKREENPYD: 780	720 MILFGEEDVRVANLKPRISENFFVTA, KRVSDIIPRTEVEKAIRMSRSRINDAFRLNDI :	630 640 LIGDKAYEWNDNEM LI	540 550 560 570 splhkcdisnsteaggklenmlrigksepwitalenvygj	490
	790 SIDISKGENN SMDIGKGESN 790	720 INDAFRLNDN 	O MYLERSSVA : MFLERSSVA	570 LALENVVGA EALENVVGA	500

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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4291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            908470 segs, 133250620 residues
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// SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT: *
// SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT: *
// SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT: *
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _Geneseq__101002:*
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and is derived by analysis of the total score distribution. pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

SUMMARIES

Result No.

Score

Query Match Length DB

core	Match	Match Length DB ID	₽B		PCT PS	Description	F. 19.
4291	100.0	805	21	AAY84562	05-04-2000	A human angiotensi 30	
4291	100.0	805	21	$^{\circ}$	22-01-184		
4291	100.0	805	22				
4291	100.0	805	22	AAB48095		Human Zace2 protei	
4291	100.0	805	23	AAU99701		Human angiotensin	
4291	100.0	805	23	AAE20353		Human ACE-2 full-1	
3775	88.0		22	AAU09092		Novel human protei	¥
3579	83.4	805	22	AAB48097		Mouse Zace2-5 prot	
3561	83.0	805	22	AAB48098		Mouse Zace2-10 pro	
2979	69.4	555	22	AAU12207		Human PRO1885 poly	

888888888888	2539 59.2 1359 31.7 1344 31.2 1337 31.2 1337 31.2 1336 31.1 1336 31.1 1334 31.1 1334 31.1 1086 25.3 1028 24.0 990 23.1 990 23.1 990 23.1 990 23.1 990 23.1 19.6 19.6 19.6 19.6 19.6
3 250 233 250 233 250 233 250 232 230 250 252 250 252 250 252 250 252 250 252 250 252 252	480 261 732 1265 1306 1306 1306 1249 1252 615 660 630 630 630 634 634
3 AAO20950 3 ABO20950 2 ABB59152 2 ABB59496 2 AAB88580 9 AAY29670 9 AAY29653 0 AAY259653 0 AAY259653 0 AAY259650 0 AAY358450 0 AAY358450 0 AAY12986 0 AAY12986 0 AAY12986 0 AAY12986 1 AAY011594 1 AAY011594 1 AAG0011594 1 AAG0011594 1 AAG0011594	
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ALIGNMENTS

RESULT 1 AAY84562 A human angiotensin converting enzyme-2 (ACE-2) protein. 25-JUL-2000 (first entry) AAY84562; AAY84562 standard; Protein; 805 AA.

Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9); BIGGO pressure; hypertension; congestive hears failure; atherosclerosis; chronic heart failure; acute heart failure; myocardial infarction; renal failure.

Homo sapiens.

ET Serves ET FT XX XX CGG Domain Domain Domain Domain Peptide Key 19.740 /note= "extracellular domain" 374..378 741..765 /note= "transmembrane domain" 766..805 Location/Qualifiers /note= /note= "signal sequence" note= "minimal zinc binding domain" "cytoplasmic domain"

WO200018899-A2

06-APR-2000

29-SEP-1999;

99WO-US22976.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a human angiotensin converting enzyme-2 (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The sequence of the full length ACE-2 CDNA was determined from a clone obtained from a CDNA library prepared from mRNA of a human heart of a subject who had congestive heart failure. ACE-2 has significant sequence homologies with ACE enzymes, and has also been shown to hydrolyse angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat blood pressure related diseases and conditions, such as hypertension, congestive heart failure, chronic heart failure, acute heart failure, myocardial infarction, atherosclerosis and renal
                                                                      481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                                                                                                                          361
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KCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK
                                                                                         KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
                                                                                                                                                                                                                                                                                           KREIVGVVEFVFHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
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                                                                                                                                                                         IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM
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NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120

MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60

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                                                              Query Match
                                                                                                                                                                       This is amino acid sequence #1 of human MPROT15. The MPROT15 polynucleotide and polypeptide sequences can be used for the treatment of hypertension, myocardial diseases, apoplexy, heart diseases, nervous denaturation, Alzheimer's disease and diseases related to the processing of peptide hormones and cytokines.
                                                                                                                                                                                                                                                                                                                                                                                               MPROT15 polypeptide and MPROT15 polynucleotides - useful for the treatment of hypertension, myocardial diseases, apoplexy, heart diseases, nervous denaturation, Alzheimer's disease etc.
                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 15; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-109268/10.
N-PSDB; AAZ59465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPROT15; treatment; hypertension; human; myocardial disease; apoplexy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM PLC
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18-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human MPROT15 amino acid sequence
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tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481
                                                                                                                            Human angiotensin converting enzyme-2 (ACE-2).
                                                                                            Human; angiotensin converting enzyme-2; ACE-2; peptidyl dipeptidase screening; therapy; hypertension; congestive heart failure; CHF;
                                                                                                                                                      31-MAY-2001
                                                                                                                                                                                                                                                     781
                                                                Homo sapiens
                                                                                   inflammation; pain
          Protein
                              Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                           KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS
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                                                                                                                                                       (first entry)
                              Location/Qualifiers
/label= Signal_peptide
19..805
/label= Mature_ACE-2_protein
                                                                                                                                                                                                   805 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 805;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present amino acid sequence is human angiotensin converting enzyme-2 (ACE-2), also referred as peptidyl dipeptidase A (EC 3.4.15.1). Nucleic (ACE-2), also referred as peptidyl dipeptidase A (EC 3.4.15.1). Nucleic acid sequence encoding ACE-2 is useful as antisense or antigene agents for sequence specific modulation of gene expression or in the analysis of sequence specific mutations in the gene. Nucleic acid sequence encoding single base-pair mutations in the gene. Nucleic acid sequence encoding ACE-2 is useful in therapeutics, diagnostics and in screening assays. ACE-2 antagonist is used to treat hypertension or congestive heart ACE-2 antagonist is used to reduce the inflammation and pain resulting from an insect sting or bite, which was accompanied by an injection of bradykinin. Anti-ACE-2 antibodies are used to monitor ACE-2 injection for determining the disease or condition associated with a horizont rectain levels for determining the disease or condition associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-210604/21.
N-PSDB; AAD02758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acton SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 33; Fig 1; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel genes encoding angiotensin converting enzyme-2 useful as antisense or antigene agents for therapeutics, diagnostics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                screening assays -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an aberrant protein level.
                                                                                                                                                                                                                                         121 NTMSTIYSTGKYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEYGKQLRPLY 180
301 AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM 360
                301 AWDAQRIFKEAEKFFVSVGLPNWTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM 360
                                                                  241 HAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQ
                                                                                    241 HAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGOKPNIDVTDAMVDO
                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                              1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60
                                                                                                                                      EEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHL
                                                                                                                                                                                                          NTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY
                                                                                                                                                                                                                                                                                                           NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
                                                                                                                                                        EEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHL
                                                                                                                                                                                                                                                                            NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSYLSEDKSKRLNTIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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/label= TMD
/note= "Transmembrane domain; Hydrophobic region"
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/label= ZBD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "zinc binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Cytoplasmic_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 4291; 100.0%; Pred. No. 0;
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RESULT 4
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                                     Angiotensin-converting enzyme, Zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases
 Example 1; Page 95-100; 125pp; English.
                       associated with inflammation such as arthritis and enterocolitis
                                                                                          N-PSDB; AAC84366, AAC84367.
                                                                                                             WPI; 2001-025018/03
                                                                                                                                         Piddington CS,
                                                                                                                                                                                                                                                                                                                                             Zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility; zinc metallopeptidase; blood pressure; zinc protease; hypertension; ventricular systolic dysfunction; renal impairment; heart failure; scleroderma renal crisis; atherosclerosis; antiinflammatory; human; antiarthritic; bradykinin inactivator.
                                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                               13-MAY-1999;
27-AUG-1999;
                                                                                                                                                                                                                                              03-MAY-2000;
                                                                                                                                                                                                                                                                                                      W0200070032-A1
                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Zace2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB48095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB48095 standard; Protein; 805 AA
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                                                                                                                                                                                                                                         2000WO-US11932
                                                                                                                                      Petrie CR,
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99US-0384706.
                                                                                                                                  Shoemaker KE,
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                        661 QMILFGEEDVRVANLKPRISFNFEVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDN
                                                                                                                                                               541 KCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNNVRPLLNVFEPLFTWLKDQNK 600
                                                                                                                                                                                                                                         481 KREIVGVVEPVPHDETYCDPASLEHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH 540
                                                                                                                                                                                                                                                                                              421 IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM
                                                                                                                                                                                                                                                                                                                                                                                            361
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                                                                                                                                                                                                                                                                                                                                                                                                          361 CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AWDAQRIFKEAEKFFVSVGLPNWTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 HAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-converting enzyme is a zinc metallopeptidase that plays roles in blood pressure regulation and fertility. Zace2 can be expressed by standard recombinant methodology. Zace2 polypeptides are useful for treating an inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), and diseases associated with inflammation like arthritis and enterocolitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infertility. The present sequence represents the human Zace2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as targets for identifying modulators of zinc protease activity, for screening or identifying new angiotensin-converting enzyme (ACE) inhibitors, and as a basis for rational drug design for inhibitory molecules. The nucleic acids can be used to detect the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NMNNAGDKWSAFIKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60
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                                                               NSFVGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKN
                                                                                                  NSFYGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKYKN 660
                                                                                                                                                                                                                  KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH 540
                                                                                                                                         KCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK 600
CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                805;
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Pred. No. 0;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurodegenerative disorder; peptide hormone; cytokine processing; myocardial infarction; cardiomyopathy; inflammatory bowel disease; systemic inflammation response syndrome; polytrauma; pain; stroke; bone destruction; rheumatoid arthritis; osteoarthritis; asthma; periodontal disease; dysmenorrhoea; premature labour; brain oedema; focal injury; diffuse axonal injury; reperfusion injury; scar formation; cerebral vasospasm; subarachnoid haemorrhage; allergic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              muscle mass; body fat; obesity; diabetes; atherosclerosis; weight loss; lipid metabolism; weight gain; anorexia; cachexia; bulimia; sepsis; familial partial lipodystrophy; hypercholesterolaemia; hyperlipidaemia; aberrant metabolic rate; heart failure; left ventricular hypertrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU99701 standard; Protein;
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The present invention describes a new method of treating a body weight disorder, increasing muscle mass and decreasing body fat by administration of angiotensin converting enzyme (ACE)-2 modulating compound. The invention can be used for treating body weight disorders, particularly obesity of at least grade 1, diabetes, atherosclerosis and a state associated with lipid metabolism. The method is used for treati
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                                                                                                                                                                                                                                                                                                         administering angiotensin converting enzyme-2 modulating
                                                                                                                                                                                                                                                                                                                       Treating body weight disorder and increasing muscle mass comprises administering angiotensin converting enzyme-2 modulating compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-2000: 2000HS-0704216.
29-MAY-2001; 2001US-0870382.
19-OCT-2001; 2001US-371741P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                      Example 5; Page 387-390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dult respiratory distress syndrome; wound healing; appetite;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and periodontal disease, dysmenorrhoea, premature labour, brain oedema following focal injury, diffuse axonal injury, stroke, reperfusion injury, cerebral vasospasm after subarachnoid haemorrhage, allergic disorders including asthma, adult respiratory distress syndrome, wound healing and scar formation. The invention decreases the appetite, increases muscle mass and decreases body fat of subject having body mas index of greater than 23 (preferably 24.9)kg/m^2. The present amino acid sequence represents the human ACE-2 protein of the invention.
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                  QMILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDN 720
                                                                                              NSFVGWSTDWSDYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKN
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      The invention relates to human angiotensin converting enzyme-2 (ACE-2) polypeptides and polypuclotides. ACE-2 is also known as peptidyl dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for treating or preventing the development of abnormal blood pressure and diseases or disorders associated with the protein in a subject. The diseases include hypertension, hypotension, congestive heart failure, chronic heart failure, acute heart failure, myocardial infarction, atherosclerosis, arrhythmia and renal failure. They are also useful for treating inflammatory conditions and diseases relating to fertility. The present sequence is human full-length ACE-2 protein.
                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 1; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      Isolated human polypeptide, known as angiotensin converting enzyme-2, useful for treating or preventing the development of an abnormal bloopressure or related diseases, e.g. hypertension, heart failure or myocardial infarction -
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Novel human protein NHP #1

20-DEC-2001

(first entry)

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Huntington's disease; schizophrenia; mania; dementia; paranoia; panic disorder; learning disability; amyotropic lateral sclerosis; psychosis; autism; sleep disorder; imunune system disorder; Hashimoto's thyroiditis; musculo-skeletal system disorder; multiple sclerosis; ischaemic brain injury; stroke; infectious disease; diabetes mellitus; immunological disorder; asthma; AIDS; immunogen; acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis; inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus; neural system disorder; respiratory disorder; oifactory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyperproliferative disorder; pulmonary system disorder; central nervous system disorder; bone disorder; neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastrointestinal disorder; cardiovascular disorder; hypertension; coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypotensive; anorectic; antiinfertility; neuroleptic; anticonvulsant; antinanic; immunosuppressive; cerebroprotective; antimicrobial; antiinflammatory; antibacterial; antipsoriatic; thyromimetic; immunomodulator; antiseborrheic; dermatological; vasoconstriction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; novel human protein; NHP; antidiabetic; antirheumatic; antiarthritic; cytostatic; antiarteriosclerotic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroprotective; nootropic; antiparkinsonian;
anti-human immunodeficiency virus; antiasthmatic; vasotropic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cachexia; male infertility; impotence; testicular cancer; lung tumour;
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29-SEP-2000; 2000US-236384P.
                                                                                                                   N-PSDB; AAS14880.
                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                      02-APR-2001; 2001WO-US10542
                                                                                                                                                                                                                                                                                                                                          11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                           WO200174896-A1
                Claim 11; Page 298-301; 318pp; English
                                               disorders, autoimmune disorders and reproductive disorders
                                                               New human proteins, useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cardiovascular
                                                                                                                                     WPI; 2001-626394/72.
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                                                                                                                                                                        Dillon PJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Immunogenic_epitope
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                                                                                                                                                                                                                                                                                                                                                                                                               /label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                              'label= OTHER
'note= "Other= Any amino acid encoded by NTT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label= Immunogenic_epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (e.g. male infertility and/or impotence), testicular cancer, lung tumours and other hyperproliferative disorders, disorders of pulmonary system, central nervous system disorders, bone disorders, neurodegenerative diseases and behavioural disorders (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, schizophrenia, mania, dementia, paranoia, panic disorder, learning disabilities, amyotropic lateral sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sepsis, acne, psoriasis and lupus erythematosus), neural system disorders, respiratory disorders, olfactory disorders and wound healing. The present sequence represents an NHP of the invention the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               brain injury and/or stroke), infectious diseases, diabetes mellitus, immunological disorders (e.g. asthma, acquired immunodeficient syndrome (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease, (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    psychoses, autism, sleep disorders), immune system disorders (e.g. Hashimoto's thyroiditis), renal and musculo-skeletal system disorders, central nervous system disorders (e.g. multiple sclerosis, ischaemic
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                                                                                                                                                                                                                                                                                                                                                                                                                             301 TKVTNDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC
662 MILFGEEDVRVANLKDRISENFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNS 721
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                                                                  62 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 121
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                                                                                                                                                                                                                                                                                                                                                                                  GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK
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                                                                                                                                                          CDISNSTEAGQKLFNMLRXGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 540
                                                                                                                                                                                                                                                                         REIVGVVEPVDHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK 541
                                                                                                                                                                                                                                                                                                                                       SFVGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQ 661
                                                                                                                                                                                                     CDISNSTEAGOKLFNMLRIGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN 601
                                                                                                                                                                                                                                               REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK
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1; Mismatches 4; 7 Indels 0
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RESULT 8
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The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-converting enzyme is a zinc metallopeptidase that plays roles in blood pressure regulation and fertility. Zace2 can be expressed by standard recombinant methodology. Zace2 polypeptides are useful for treating an inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), as targets for identifying modulators of zinc protease activity, for screening or identifying new angiotensin-converting enzyme (ACE) inhibitors, and as a basis for rational drug design for inhibitory modecules. The nucleic acids can be used to detect the expression of a
                                                                                                                                                                                Angiotensin-converting enzyme, zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases associated with inflammation such as arthritis and enterocolitis -
                                                                                                                                                            Claim 7; Page 104-109; 125pp;
                                                                                                                                                                                                                                              N-PSDB; AAC84368, AAC84369.
                                                                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                            27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                        13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                  03-MAY-2000; 2000WO-US11932
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99US-0384706
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133..542
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YASIDISKGENNPGFQNTDDVQTSF 805
                                SLEFLGIHPTLEPPYQPPYTIWLIIFGVVMALVVVGIIILIVTGIKGRKKKNETKREENP
                                                                 SLEFLGIQPTLGPPNQPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARSGENP
                                                                                                          QTVPFLEEDVRVSDLKPRVSFYFFVTSPQNVSDVIPRSEVEDAIRMSRGRINDVFGLNDN
                                                                                                                               NSFYGWNTEWSPYADQSIKVRISLKSALGANAYEWTNNEMFLFRSSVAYAMRKYFSIIKN
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RESULT 9
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diseases associated with inflammation like arthritis and enterocollits, as targets for identifying modulators of zinc protease activity, for screening or identifying new angiotensin-converting enzyme (ACE) thibitors, and as a basis for rational drug design for inhibitory molecules. The nucleic acids can be used to detect the expression of a Zace2 gene in a biological sample, as probes for in vivo diagnosis and Zace2 gene in a biological sample, as probes for in tissue samples, to detecting and localizing Zace2 gene expression in tissue samples, to detecting and localizing Zace2 gene expression in the zace2 gene, and to detect aberrations associated with the Zace2 locus. Inhibitors of ACE are used for treating hypertension of various conditions, including left ventricular systolic dysfunction, progressive
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27-AUG-1999;
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                                                                                                                                                                                      The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin converting enzyme is a zinc metallopeptidase that plays roles in blood pressure regulation and fertility. Zace2 can be expressed by standard recombinant methodology. Zace2 polypeptides are useful for treating an inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis).
                                                                                                                                                                                                                                                                                          Claim 7; Page 113-118; 125pp; English.
                                                                                                                                                                                                                                                                                                                        Angiotensin-converting enzyme, Zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases associated with inflammation such as arthritis and enterocolitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                              Piddington CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO ) ZYMOGENETICS INC
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99US-0384706
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19..70
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              systolic dysfunction, progressive
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                                                                                                                             QTVPFLEEDVRVSDLKPRVSFYFFVTSPQNVSDVTPRSEVEDAIRMSRGRINDVFGLNDN
                                                                                                                                                                                                 NSFYGWNTEWSPYADQSIKVRISLKSALGANAYEWTNNEMFLFRSSVAYAMRKYSSIIKN
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                                                                                             SLEFTGIOPTLGPPNOPPVSIWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARSGENP
                                                                                                                                                             QMILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDN 720
   YDSMDIGKGESNAGFQNSDDAQTSF
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RESULT 10

AAU12207;

AAU12207 standard;

Protein;

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AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from
                                                                                                                                                              Claim 12; Fig 72; 813pp; English.
                                                                                                                                                                                            Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-2000
22-FEB-2000
24-FEB-2000
24-FEB-2000
01-MAR-2000
20-MAR-2000
30-MAR-2000
31-MAR-2000
31-MAR-2000
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11-FEB-2000;
18-FEB-2000;
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                                                                                                                                                                                                                                                                                                             Gerritsen
                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
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                                                                                                                                                                                          breast, prostate, cervical
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2000WO-USO8439
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2000WO-US07377.
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2000WO-US04342.
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                                                                                                                                                                                                                                                                                         D, Watanabe CK,
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L, Sherwood S;
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                                        Alzheimer's disease; cytokine.
                                             MPROT15; treatment; hypertension; human; myocardial disease; apoplexy;
heart disease; apoplexy; heart disease; nervous denaturation; hormone;
                                                                                                                                            11-APR-2000 (first entry)
                                                                                                          Human MPROT15 amino acid sequence #2
                                                                                                                                                                                                              AAY67311 standard; Protein; 480 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA, The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                    541 KCDISNSTEAGOKL 554
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                                                                                                                                                                                                                                                                                                                                                           KREIVGVVEPVPHDETYCDPASLFHVSDDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
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                                                                                                                                                                                                                                                                                                                                                                                                                               IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \tt AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NMNNAGDKWSAFIKEOSTLAOMYPLOEIQNLTVKLOLQALQQNGSSVLSEDKSKRLNTIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  555 AA;
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99.8%;
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Pred. No. 3.8e-244;
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Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP11318472-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is amino acid sequence #2 of human MPROT15. The MPROT15 polynucleotide and polypeptide sequences can be used for the treatment of hypertension, myocardial diseases, apoplexy, heart diseases, nervous denaturation, Alzheimer's disease and diseases related to the processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases, nervous denaturation, Alzheimer's disease etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-109268/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 19; Page 20-21; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPROT15 polypeptide and MPROT15 polynucleotides - useful for the treatment of hypertension, myocardial diseases, apoplexy, heart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of peptide hormones and cytokines.
                                                                                                                                                                                                                                                                                                                                                                                                                                130
                                                                                                                                                                                                                                                                                                                                                                                                                                                           131
                                                                               AAU09102 standard; Protein; 261 AA.
                                                                                                                                                                                                                                                                                                                                                                        190 ARANHYEDYGDYWRGDYEVNGVDGYDYSRGOLIEDVEHTFEEIKPLYEHLHAYVRAKLMN
                                                                                                                                                                                                                                                                                                                                                                                                    191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310
                                                                                                                                                                                                                                                                                      311 AEKFFYSYGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFL 370
                                                                                                                                                                                                                                                                                                                  250 AYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 309
                                                                                                                                                                                                                                                                                                                                         251 AYPSYISPIGCLPAHLLGDMWGREWTNLYSLTVPFFGQKPNIDVTDAMYDQAWDAQRIFKE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 AFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSYLSEDKSKRLNTILNTMSTIYSTG 130
Novel human protein NHP #11.
                             20-DEC-2001
                                                      AAU09102;
                                                                                                                                                                            431 DNETEINFLLKQALTIVGTLPETYMLEKWRWMVEKGEIPKDQWMKKWWEMK 481
                                                                                                                                                                                                        370 TAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQE
                                                                                                                                                                                                                               371 TAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDEQE 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                   430 DNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 480
                                                                                                                                                                                                                                                                                                                                                                                                                             KYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKOLRPLYEEYVVLKNEM 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFLKEQSTLAQMYPLQEIONLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTG 129
                                                                                                                                                                                                                                                                                                                                                                                                 ARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMN 250
                                                                                                                                                                                                                                                             AEKFEVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFL
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98GB-0018009.
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                             (first entry)
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hyperpoliferative disorder; pulmonary system disorder; hyperpoliferative disorder; bone disorder; barkinson's disease; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; nuntington's disease; Schizophrenia; mania; dementia; paramoia; panic disorder; learning disability; amyotropic lateral sclerosis; panic disorder; learning disability; amyotropic lateral sclerosis; panic disorder; musculo-skeletal system disorder; psychosis; attism, sleep disorder; immune system disorder; multiple sclerosis; ischaemic brain injury; stroke; infectious disease; multiple sclerosis; ischaemic brain injury; stroke; infectious disease; multiple sclerosis; inmunological disorder; asthma; AIDS; immunogen; diabetes mellitus; immunological disorder; asthma; AIDS; immunogen; inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus; inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus; neural system disorder; respiratory disorder; olfactory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; novel human protein; NHP; antidiabetic; antirheumatic; antiarthritic; cytostatic; antiarteriosclerotic; vulnerary; neuroprotective; nootropic; antiparkinsonian; anti-human immunodeficiency virus; antiasthmatic; vasotropic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastrointestinal disorder; cardiovascular disorder; hypertension; coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia; cachexia; male infertility; impotence; testicular cancer; lung tumour cachexia; male infertility; impotence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antimanic; immunosuppressive; cerebroprotective; antimicrobial; antinflammatory; antibacterial; antipsoriatic; thyromimetic; immunomodulator; antiseborrheic; dermatological; vasoconstriction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypotensive; anorectic; antiinfertility; neuroleptic; anticonvulsant;
WO200174896-A1
                                                                                                                                                                                                                 wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lung tumour;
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Homo sapiens.

02-APR-2001; 2001WO-US10542.

03-APR-2000; 29-SEP-2000; 2000US-194118P. 2000US-236384P.

(HUMA-) HUMAN GENOME SCI INC

Moore PA, PA, Ni J, Dillon PJ; Soppet DR, Coleman TA, Gentz RL, Endress GA;

N-PSDB; AAS14890. 2001-626394/72.

prognosing disorders related to the proteins, including car disorders, autoimmune disorders and reproductive disorders New human proteins, useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cardiovascular

Claim 11; Page 311-312; 318pp; English.

The invention relates to novel human proteins (NHP) and the conveled acids that encode them and antibodies raised against them. CC nucleic acids that encode them and antibodies raised against them. CC prognosis, prevention and/or treatment or diseases and/or disorders cc prognosis, prevention and/or treatment or diseases and/or disorders cc prognosis, prevention and/or treatment or diseases and/or disorders cc disorders (e.g. hypertension, erectile dysfunction, high blood pressure, cc disorders (e.g. hypertension, erectile dysfunction, high blood pressure, cc coronary heart disease and arteriosclerosis), anorexia, obesity, bulimia, cc coronary heart disorders of small intestine, disorders of reproductive system cc cathexia, disorders of small intestine, disorders of pulmonary system, cc disease, and behavioural disorders, disorders, neurodegenerative cc disease, huntington's disease, schizophrenia, mania, dementia, paramoia, cc disease, huntington's disease, schizophrenia, mania, dementia, paramoia, cc disease, huntington's disease, schizophrenia, mania, dementia, paramoia, cc psychoses, autism, sleep disorders), immune system disorders (e.g. psychoses, autism, sleep disorders), immune system disorders (e.g. psychoses, autism, sleep disorders), immune system disorders, cc panic disorder, learning disorders, learning disorders, celectous disorders, ischaemic cc entral nervous system disorders (e.g. multiple sclerosis, ischaemic cc immunological disorders (e.g. asthma, acquired immunodeficient syndrome immunological disorders (e.g. asthma, acquired immunodeficient syndrome communological disorders (e.g. asthma, acquired immunodeficient syndrome sepsia, acne, psoriasis and lupus erythematosus), neural system cc disorders, respiratory disorders, olfactory disorders and wound

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A bank of human testicular cDNA in Lambda gtll was screened with a probe containing the final 3248 nucleotides of endothelial ACE. The complete sequence of tACE was reconstructed from 4 separate clones.
                                                                                                                         Claim 1; Fig 1; 48pp; French.
                                                                                                                                                         Nucleic acid - encoding human testicular angiotensin conversion enzyme, used e.g. for in vitro detection of enzyme in organism
                                                                                                                                                                                                                                                                          N-PSDB; AAQ10328
                                                                                                                                                                                                                                                                                                                                   Soubrier F, Alhenc-Gelas F, Hubert C,
                                                                                                                                                                                                                                                                                              WPI; 1991-036748/05.
                                                                                                                                                                                                                                                                                                                                                                                              (INRM ) INST NAT SANTE RECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human testicular angiotensin conversion enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 WDAQRIFKEAEKF 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 WDAQRIFKEAEKF 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 AYVRAKLMNAYDSYISPIGCLPAHLLGDMWGRFWTNLYSLTVDFGQKPNIDVTDAMVDQA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 EYVVLKNEMARANHYEDYGDYWRGDYEVNGYDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 TMSTIYSTGKYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 120
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99.6%;
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Pred. No. 5.3e-107;
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640 LHGEKLGWPQYNWTPNSARS 659
                                   601 --NSFVGW-STDWSPYADQS 617
                                                                                       541 KCDISNSTEAGOKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNVFEPLFTWLKDONK 600
                                                                                                                               520 RLKYQGLCPPVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLH 579
                                                                                                                                                                 481 KREIVGVVEFVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH 540
                                                                                                                                                                                                     461 LNLLSSEGGSD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSL 519
                                                                                                                                                                                                                                         421 IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM 480
                                                                                                                                                                                                                                                                             401 CTTVNLEDLVVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHS 460
                                                                                                                                                                                                                                                                                                   361 CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
                                                                                                                                                                                                                                                                                                                                                     341 WTPRRMFKEADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQ
                                                                                                                                                                                                                                                                                                                                                                                       302 WDAQRIFKEAEKFFVSVGLDNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DERILM 360
                                                                                                                                                                                                                                                                                                                                                                                                                          281 YVRRALHRHYGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVFFPSAPSMDTTEAMLKQG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 YVRAKLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 YVELINQAARLNGYVDAGDSWRSMYETPSLE------QDLERLFQELQPLYLNLHA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 YVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 METTYSVATVCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWBGWRDKAGRAILQFYPK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The isolated nucleic acid sequence was inserted into a plasmid for expression of the protein. The invention covers polypeptides containing all or part of tACE sequence. These are useful in part of inflammation or infectious diseases, especially acute pancreatitis, or diseases in which kinins are involved. Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 MSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWBSWRSEVGKQLRPLYEE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NHT-----LKYGTQARKEDVNQLQNTTIKRIIKKVQDLERAALÞAQELEEYNKILLD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 against the polypeptides are useful as immunoassay reagents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 NNAGDKWSAFLKEOSTLAOMYPLOEIONLTVKLOLOALOONGSSVLSEDKSKRLNTILNT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TSAQSPNIVTDEAEASKEVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 TAAQS----TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNM 62
                                                     KCDIYQSKEAGORLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENE 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.3%; Score 1344; DB 12; Length 732; Conservative 119; Mismatches 204; Indels 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   732 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Gaps
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RESULT 14
AAO20501
ID AAO20501 standard; Protein; 1265 AA.

AC AAO20501;
XX
DT 27-JUN-2002 (first entry)
XX
DT 27-JUN-2002 (first entry)
XX
Ext
Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta; KW amyloid precursor protein; tissue-specific expression control; human App; XX
APP pathway modulator; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2001; 2001WO-EP11345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200226820-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-SEP-2000;
14-JUN-2001;
                                                                                                                                                                                                                                                                                                                                        specific expression control sequence. Expression of the sequence gives the fly an altered phenetype. The purpose of the invention is for identifying agents that inhibit or promote the expression and/or function of genes or encoded polypeptides which modify the APP pathway. The agent is a compound, triple helix DNA, antisense oligonucleotide, double stranded RNA molecule, ribozyme, or particularly an antibody. It is used stranded RNA molecule, ribozyme, or particularly an antibody. It is used as to treat conditions such as Alzheimer's disease. The agent can be used as to pathway modulator or in gene therapy. This sequence represents the protein of the APP related human homologue hCP51674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a transgenic fly whose genome comprises DNA encoding a polypeptide having the Abeta portion of human amyloid encoding a polypeptide having the Abeta portion of human amyloid encoding a polypeptide having the Abeta portion of human amyloid encoding polypeptide having the a signal sequence. The DNA sequence is a signal sequence, given it the specification. The DNA sequence is operably linked to a tissue-the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transgenic fly, containing DNA encoding an Abeta portion of human APP, useful for identifying agents which modulate the APP pathway and which can be used to treat Alzheimer's disease \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reinhardt MWHM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVS ) NOVARTIS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 94-97; 129pp; English.
                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                       603 TDEAEASKEVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT----- 656
                                                                                                                       132 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYYVLKNEMA 191
                                                                                                                                                 657 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 714
                                   773 RLNGYVDAGDSWRSMYETPSLE------QDLERLFQELQPLYLNLHAYVRRALHRH 822
             252
                                                                                                                                                                                                                                20 TIEEQAKTELDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNMNNAGDKWSA 71
                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-315796/35.
                                                               RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 251
                                                                                                                                                                            FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 131
                                                                                          VCHPNG--SCLQLEPDLINVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 772
          Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK99395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dengler UJ,
                                                                                                                                                                                                                                                                                                                      1265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001US-298309P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-236893P
                                                                                                                                                                                                                                                               Conservative 118; Mismatches 204;
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/note= "Encoded by CNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Encoded by TGN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zusman S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= unknown
                                                                                                                                                                                                                                                                              31.2%; Score 1337; DB 23; Length 1265; 41.7%; Pred. No. 4.6e-104;
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       1::1 1:11: 1 - :1:11
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                                                                                                                                                                                                                                                                           34;
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AAR04111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          823 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1122 AGORLATAMKLGFSRPWPBAMOLITGOPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1062 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       943 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            883 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 AEKEFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR04111 standard; peptide; 1306 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1182 QYNWTPNSARS 1192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              490 PVPHDETYCDPASLFHVSNDYSFIRYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               430 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human angiotensin converting enzyme (ACE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR04111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              550 AGOKLENMLRLGKSEPWILALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human angiotensin converting enzyme; hypertension; bradykinin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=putative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="derived from pre-ACE by removal of signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=mature ACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label-putative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label=putative N-glycosylation site
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                                                                                                                                                                                                                                                                                                                                                                                                                    /label=putative N-glycosylation site
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/label=putative N-glycosylation site
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                                                                                  'label=putative N-glycosylation site
                                                                                                                        _putative N-glycosylation site
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Matches 255;
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                                   1103 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 1162
550 AGOKLFUMLRIGKSEFWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDONK--NSFVGW- 606
                                                                                                     1044 SD-EHDINFLMKMÁLDKTAFTPFSYLVDQWRWRVFDGSTTKENYNQEWNSLRLKYQGLCP 1102
                                                                                                                                      430 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 489
                                                                                                                                                                          984 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 1043
                                                                                                                                                                                                370 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 429
                                                                                                                                                                                                                                               924 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 983
                                                                                                                                                                                                                                                                               311 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRTLMCTKVTMDDF 369
                                                                                                                                                                                                                                                                                                                  864 YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEANLKQGWTPRRMFKE 923
                                                                                                                                                                                                                                                                                                                                                252 Y-PSYISPIGCLPAHLLGDMWGREWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 310
                                                                                                                                                                                                                                                                                                                                                                                        814 RLNGYVDAGDSWRSMYETPSLE------QDLERLFQELQPLYLNLHAYVRRALHRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human angiotensin converting enzyme hydrolyses angiotensin I and kinins. Either intact enzyme or fragments thereof can be used to generate antibodies for diagnostic use. Oligonucleotide probes can also be made
                                                                                                                                                                                                                                                                                                                                                                                                                        192 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                         756 VCHPNG--SCLQLEPDLTNYMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             698 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which are complementary to the sequence encoding the enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; ; p; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA encoding human angiotensin converting enzyme used eg in diagnosis of hypertension, evaluation of enzyme inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              644 TDEAEASKEVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNWQIANHT----- 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-132272/17.
N-PSDB; AAQ04027.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INRM ) INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 FLKEQSTLAOMYPLQEIONLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNMNNAGDKWSA 71
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                                                                   PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88FR-0012620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=putative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=putative N-glycosylation site
1225..1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.2%; Score 1337; DB 11; 41.7%; Pred. No. 4.8e-104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hubert C, Corvol P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Sequence

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C resulting in 3 genotypes, II, ID and DD. It is an object of the CC invention to identify individuals possessing a certain genotype and CC individual can be improved by altering behavior. A claimed method comprises identifying individuals having a certain phenotype, and the theorem of the presence or absence of genetic markers associated CC with the phenotype, and instituting a lifestyle change to exploit CC with the phenotype, and instituting a lifestyle change to exploit CC phenotype is hypertension, the gene marker if the CC insertion (I) ACE allele and exercise training is instituted to CC can be identified by PCR amplification (see AAVA1321-22) of the CC identify subjects who will benefit most from physical exercise CC and also to identify those who are likely to be successful in CC sports.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is human angiotensin converting enzyme (ACB). (see AAV41320) is polymorphic with 2 common alleles resulting in 3 genotypes, II, ID and DD. It is an olinvention to identify individuals possessing a certainvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 35-41; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      angiotensin-converting enzyme genotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Analysis of genetic markers to identify subjects who will benefit from exercise - also assessing risk of cardiovascular disease from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV41320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ferrell RE, Hagberg JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAY-1997;
16-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human angiotensin converting enzyme.
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Length 1306;

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Matches 255; Conservative 118; Mismatches
                                                                                                                    Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1044
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                                                                                                                                                                                                                                                                                                                          Angiotensin converting enzyme (ACEV) splice variant protein #57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU02957 standard; Protein; 1249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                   vascular disorder; asbestosis.
                                                                                                      nonarcoidotic pulmonary granulomatous disease; endothelial abnormality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLNGYVDAGDSWRSMYETPSLE-----QDLERLFQELQPLYLNLHAYVRRALHRH 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCHPNG--TCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 1162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 1222
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The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                               Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-NOV-2000; 2000WO-IL00766
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                                 disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases suc as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-1999;
                                                                                                                                                                       polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various
                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Fig 57; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS06057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Levine Z, David A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COMP-) COMPUGEN LTD
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99IL-0133455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Khosravi R,
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Sequence 1249 AA;

Query Match

Length 1249;

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            767 TCMPLEPDLTNMMATSRKYEELLWAWKSWRDKYGRAILPFFPKYVEFSNKIAKLNGYTDA 826
997 HIQYEMQYKDLPVTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 TIREQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKTFDVSNFQNSSIKRIIKKLQNLDRAVLPPKELEEYNQILLDMETTYSLSNICYTNG-- 766
                                                     HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 437
                                                                                                                                                                                                                                       DGPTPAHLLGNMWAQTWSNIYDLVAPFPSAPNIDATEAMIKQGWTPRRIFKEADNFFTSL 936
                                                                                                                                                                                                                                                                                                                                                     GDSWRSLYESDNLE------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL 876
                                                                                                                                                                                                                                                                                                                                                                                                             GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 258
                                                                                                                   GLLPVPPEFWNKSMLEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHEMG 996
                                                                                                                                                                            {\tt GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG}
                                                                                                                                                                                                                                                                                             IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.1%; Score 1334; DB 22; 42.6%; Pred. No. 8.1e-104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 213;
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RESULT 18
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                                                                                        The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor IC, cellular tumour antigen p53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various
                  disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis,
                                                                                                                                                                                                                                                                                                     Claim 4; Fig 85; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                      Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antiboo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; wasoactive intestinal polypeptide receptor 2; arteriasclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; multiple sclerosis; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000; 2000WO-IL00766
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10-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vascular disorder; asbestosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Angiotensin converting enzyme (ACEV) splice variant protein #85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-336004/35.
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sarcoidosis, nonarcoidotic pulmonary granulomatous diseases
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99IL-0133455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Azar I, Khosravi R,
                                                                                                                                                                                                                                                                                                                                                      and to detect anti-variant antibodies
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ABB64006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
23-MAR-2000;
11-JUL-2000;
                                                 23-MAR-2001; 2001WO-US09231.
                                                                                                                       WO200171042-A2
                                                                                                                                                       Drosophila melanogaster
                                                                                      27-SEP-2001
                                                                                                                                                                                              pharmaceutical.
                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 18810.
                                                                                                                                                                                                                                                                                                                                              ABB64006 standard; Protein; 615 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               1176 MKLGYSKPWPEAMKLITGOPNMSASAMMNYFKPLTEWLVTENRRHGETLGWPEYNWAP 1233
                                                                                                                                                                                                                                                                               26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                      ABB64006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIQYFMQYKDLPYTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN 1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 199
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2000US-191637P
2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1334; DB 22;
Pred. No. 8.1e-104;
2; Mismatches 213;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 18810; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 KLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 KWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIY 127
599 N--KNSFVGWST 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 LLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKVKVCDYKDSTKCDLALDPEIEEVISKSRDHEELAYYWREFYDKAGTAVRSQFERYVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLATLAVTQALVKEEIQAKEYLENLNKELAKRTNVETEAAWAYGSNITDENEKKKNEISA 67
                                                                                                                                                                                                                                                                                                                                                                                                                RLRKHYGDAVVSETGPIPMHLLGNMWAQQWSEIADIVSPFPEKPLVDVSAEMEKQGYTPL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTKAAKLNNFTSGAEAWLDEYE-----DDTFEQQLEDI---FADIRPLYQQIHGYVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STGKVCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYYVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELAKFMKEVASDTTKFQWRSYQSEDLKRQFKALTKLGYAALPEDDYAELLDTLSAMESNF 127
                                                                                                                                                                                       K-DYVRDDEARINQLFLTALDKIVFLPFAFTMDKYRWSLFRGEVDKANWNCAFWKLRDEY 476
                                                                                                                                                                                                                                                                                                TMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLL 424
                                                                                                                                                                                                                                                                                                                                        KMFQMGDDFFTSMNLTKLPQDFWDKSIIEKPTDGRDLVCHASAWDFYLTDDVRIKQCTRV
                                                                                                                                                                                                                                                                                                                                                                          RIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLG-KGDFRILMCTKV 364
                                                                       LHKCDISNSTEAGOKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQ
                                                                                                                                                   VGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALC-QAAKH-----EGP
                                                                                                                                                                                                                         SPDFQEDNETEINFLLKQALTIVGTLPETYMLEKWRWMVFKGEIPKDQWMKKWWEMKREI 484
                                                                                                               SGIEPPVVRSEKDFDAPAKYHISADVEYLRYLVSFIIQFQFYKSACIKAGQYDPDNVELP 536
                                                                                                                                                                                                                                                                TQDQLFTVHHELGHIQYFLQYQHQPFVYRTGANPGFHEAVGDVLSLSVSTPKHLEKIGLL
                                     LDNCDIYGSAAAGAAFHNMLSMGASKPWPDALEAFNGERIMSGKAIAEYFEPLRVWLEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        615 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 122; Mismatches 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.3%; Score 1086; DB 23
36.4%; Pred. No. 3.2e-83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                   598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
           RESULT 20
AAR70013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tick; antigen; carboxypeptidase; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tick carboxypeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR70013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR70013 standard; Protein; 660 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boophilus microplus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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     Clone A5 was prepd. from adult tick cDNA library. Clone 4UI was prepd. from the larval stage of B. microplus (Calliope strain).

AAQ82948 is a hybrid of sequences from clone 4UI (nt 1-966 & 1747-2047) and A5 (nts 967-1746). The translation of the tick carboxypeptidase cDNA sequence is shown in AAR70013. All the native tick carboxypeptidase sequences listed in Table 11 (see AAR70014-R70023) are found in the translation (see FT). The predicted AA sequence agrees with the peptide sequence for all peptides with 2 exceptions. These differences are Asp for Gln14 in peptide T9126, and Asn for Saspl2 in peptide T9118. Tick carboxypeptidase has a mol. wt. 75172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-FEB-1995.
                                                                                                                                                                                                                     Disclosure; Fig 6; 138pp; English.
                                                                                                                                                                                                                                                                          New antigenic tick carboxypeptidase and corresp. DNA - are used in vaccines for producing antibodies against ticks, insects and
                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ82948
                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-090905/12.
                                                                                                                                                                                                                                                                                                                                                                                            Cobon GS,
                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOT-) BIOTECH AUSTRALIA PTY LTD. (CSIR ) COMMONWEALTH SCI & IND RES ORG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                            Kemp DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93AU-0000458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= signal 639..655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= C-terminal transmembrane domain
/note= "putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label
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613 KNEVVCW 619
                                   600 KNSFVGW 606
                                                                553 HECDIYGEKNAGDVLKKGLSLGRSKPWPDVLEIMAGTROMSASSLKKYYEPLEKWLDERI 612
                                                                                          540 HKCDISNSTEAGGKLFNMLRLGKSEPWTLALENVVGAKNMVRPLLNYFEPLFTWLKDQN 599
                                                                                                                                               493 KYQGVSPPVKRNESFFDGGAKYHVALHVPYLRYFVAFILQFQFHEHLCTVAKKVDEHHPF 552
                                                                                                                                                                        483 EIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAK---HEGPL 539
                                                                                                                                                                                                                                 423 LLSPDFQEDNETEINFLLKQALTTYGTLPFTYMLEKWRWNVFKGEIPKDQWMKKWWEMKR 482
                                                                                                                                                                                                                                                                                                                 376 DPSVEELRTVHHEMGHIEYYMQYKHLHVLLQEGANEGFHEAVGDLIALSVATKTHYGKLS 435
                                                                                                                                                                                                                                                                                                                                                                                                   317 AQKMFHAAEDFFTSLGLDNMTSEFWSKSILTKPED-REIQCHASAWNMYNGDDFRIKMCT 375
                                                                                                                                                                                                                                                                                                                                                         363 KVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     In addition to the features in FT, the carboxypeptidase AA sequence has 8 potential N-lined glycosylation sites and a potential glycosylphospatidyl inositol anchor sequence similar to that found in Bm86. It has significant homology with zinc dependent dipeptidyl
                                                                                                                                                                                                                                                                                                                                                                                                                           304 AQRIFKEAEKFFVSVGLÞUMTQGFWENSMLTDDGNVQKAVCHÞTAWDLGKG-DFRILMCT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 RMKLREIYPGRLPEDGTIPAHLLGNMWAQEWGTLYPHLTME--DKP-LDISKTMVEQKWD 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 RAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLY-SLTVPFGQKPNIDVTDAMVDQAWD 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carboxypeptidases from mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 KLSNEAASLDGYDNIKSAWLSDYETE-----NMTEIVDKLWEDLSPLYKKLHAYV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 VLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGOLIEDVEHTFEEIKPLYEHLHAYV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 GSTKVTVGKDKDLP-----LEPDLTRNMKEVGNYDKLLQTWLAWHNAVGPAIKQYYIPYI 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 STGKVC---NPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 EVSKMERQFGITAKREDWHNFKNDSLKRLFRHVATIGLAALPDDKLENATSLSSKMAAIY 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 KWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 LATLSNVSALIKDEAMGVAFIEGLNDPYTTINNVDSSSSWDYASNITDYN-QNMSNKVST 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 LVAVTAAQSTIEEQAK--TFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNN-AGD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             660 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34; Gaps
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Search completed: March 13, 2003, 16:56:56 Job time: 50 secs

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OM protein - protein search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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and is derived by analysis of the total score distribution.
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4291
1 MSSSSWLLLSLVAVTAAQST......ISKGENNPGFQNTDDVQTSF 805
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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SUMMARIES

25 27 28 29	1 1 2 3 3 3 4 4 4 5 5 5 6 6 6 7 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
122 121 121 121 120	4.281 1344 1337 1337 1337 1310 1310 1310 1310 1310	Score
2222		Query Match L
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E98000 AB3511 T30574 A84683	T14762 S05238 A31759 A35655 A34171 JC2489 JC2038 A34402 S35484 S55472 A57533 JC5374 T15792 C83696 AF1310 AB1682 AF1310 B82881 B82938 AF1310 B82938 AF1310 B82938 AF1310 B82938 AF1310 B82938	ID
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SWH1 protein homol TRAP-like protein cytoplasmic dynein hypothetical prote 1,4-alpha-glucan b conserved hypothet conserved hypothet NMDA receptor-bind probable 0:1ayer p probable 0:1goendo utrophin - human thermostable carbo hypothetical prote hypothetical prote phage infection protein	

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422 GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 481	362 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 421 						Query Match 99.8%; Score 4281; DB 2; Length 804; Best Local Similarity 99.9%; Pred. No. 9.5e-288; Matches 803; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	protein DKFZp434A014.1 - human (fragment) omo sapiens (man) omo sapiens (man) r14762 r	ALIGNMENTS

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A:Cross-references: GB:M2657; NID:9338666; PIDN:AAA60611.1; PID:9338667
A:Experimental source: clones R1.2 and T8B
A:Note: neither the complete nucleic acid sequence nor the complete translation are show C:Comment: For the renal and pulmonary splice form, see PIR:A31759.
A:Genetics:
A:Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Lattion, A.L.; Soubrier, F.; Allegrini, J.; Hubert, C.; Corvol, P.; Alhenc-Gelas FBBS Lett. 252, 99-104, 1989
A;Title: The testicular transcript of the angiotensin I-converting enzyme encodes A;Reference number: S05238; MUID:89338720; PMID:2547653
A;Accession: S05238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X16295; NID:g28264; PIDN:CAA34362.1; PID:g28265
R;Ehhers, M.R.W.; Fox, E.A.; Strydom, D.J.; Riordan, J.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 7741-7745, 1989
A;Title: Molecular cloning of human testicular angiotensin-converting enzyme: the testis A;Reference number: A33979; MUID:90046671; pMID:2554286
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A; Residues: 1-732 <EHL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-732 <LAT>
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N;Alternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxypepti
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                                          259;
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                                                                    Similarity
                 Conservative 119; Mismatches
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                                                            31.3%;
                                                   Score 1344; DB 1;
Pred. No. 8.5e-85;
                                                                                 DB 1; Length 732;
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640 LHGEKLGWPQYNWTPNSARS 659
                                         601 --NSFVGW-STDWSPYADQS 617
                                                                                                           541 KCDISNSTEAGOKLFNMLRLGKSEBWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDONK 600
                                                                                                                                                         520 RLKYQGLCPPVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLH
                                                                                                                                                                                                481 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH 540
                                                                                                                                                                                                                                           461 LNLLSSEGGSD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSL 519
                                                                                                                                                                                                                                                                                  421 IGLLSPDFQEDNETEINFLLKQALTIYGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM 480
                                                                                                                                                                                                                                                                                                                              401 CTTVNLEDLVVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHS 460
                                                                                                                                                                                                                                                                                                                                                                       361 CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
                                                                                                                                                                                                                                                                                                                                                                                                                   341 WTPRRMFKEADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQ 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 WDAQRIFKEAEKFFVSVGLPNWTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILM 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 YVRRALHRHYGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 YVRAKLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 YVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 METTYSVATVCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 MSTIYSTGKYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 NNAGDKWSAFLKEQSTLAQMYPLQETQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YVELINQAARLNGYVDAGDSWRSMYETPSLE------QDLERLFQELQPLYLNLHA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NHT-----LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340
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A;Molecule type: mRNA A;Residues: 1-1306 <SOU> A;Cross-references: GB:J04144; NID:g178285; PIDN:AAA51684.1; PID:g178286 R;Soubrier, F.; Alhenc-Gelas, F.; Hubert, C.; Allegrini, J.; John, M.; Tregear, G.; Cleroc. Natl. Acad. Sci. U.S.A. 85, 9386-9390, 1988
A;Title: Two putative active centers in human angiotensin I-converting enzyme reveale A;Reference number: A31759; MUID:89071703; PMID:2849100 A;Accession: A31759 C; Accession: A31759; PQ0004 peptidyl-dipeptidase A (EC 3.4.15.1) precursor, renal and pulmonary splice form - hum N;Alternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxype C;Species: Homo sapiens (man) C;Species: 17.Jun-1990 #sequence_revision 02-Jul-1998 #text_change 18-Jun-1999

A; Experimental source: kidney
A; Note: parts of this sequence, including the amino end of the mature protein, were d
R; Takeuchi, K; Shimizu, T; Ohishi, N; Seyama, Y; Takaku, F; Yotsumoto, H.
J. Biochem. 106, 442-445, 1989
A; Title: Purification of human lung angiotensin-converting enzyme by high-performance

A; Reference number: PQ0004; MUID: 90110025; PMID: 2558109 A; Accession: PQ0004

A;Molecule type: protein A;Residues: 'XX',32-34,'E',36-37,'X',39-41,'R',43-46 <TAK> A; Experimental source: lung

A; Gene: GDB: DCP1; ACE C;Comment: This splice form is found in many tissues, in particular kidney and lung

A; Cross-references: GDB:119840; OMIM:106180

TAAQS----TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNM 62

15

protein

7;

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A;Map position: 17q23-17q23
A;Map position: 17q23-17q23
A;Bascription: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypepti A;Description: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypepti A;Note: plays a role in the control of blood pressure by catalyzing the conversion of an C;Superfamily: mammalian peptidyl-dipeptidase A
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Superfamily: mammalian peptidyl-dipeptidase F;10-130c/product: signal sequence #status predicted <SIG>F;10-130c/product: peptidyl dipeptidase I #status predicted <MANT>F;1260-1276/Domain: transmembrane #status predicted <NRNN-F;1260-1276/Domain: transmembrane #status predicted <NRNN-F;305,54,74,111,146,160,318,445,509,523,677,695,714,760,942,1191,1225/Binding site: carbo F;300,394/Binding site: zinc (His) #status predicted
F;988,992,1008/Binding site: zinc, catalytic (His, His, Glu) #status predicted
F;989/Active site: Glu #status predicted
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                                                                                     peptidy1-dipeptidase A (EC 3.4.15.1), testis - mouse
N;Alternate names: peptidy1-dipeptidase I, testis
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A35655
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R;Howard, T.E.; Shai, S.Y.; Langford, K.G.; Martin, B.M.; Bernstein, K.E. Mol. Cell. Biol. 10, 4294-4302, 1990
A;Title: Transcription of testicular angiotensin-converting enzyme (ACE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLNGYVDAGDSWRSMYETPSLE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF
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                                                                                                                                                                                                                                                                                                                                                                       QYNWTPNSARS 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                    STDWSPYADQS 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDONK--NSFVGW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 1222
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41.7%; Pred. No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----QDLERLFQELQPLYLNLHAYVRRALHRH 863
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         enzyme (ACE) is initiated
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A;Reference number: A35655; MUID:90318396; PMID:2164636
A;Accession: A35655
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-732 <HOW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:M55333; NID:g191589; PIDN:AAA37149.1; PID:g191590 C;Superfamily: mammalian peptidyl-dipeptidase A C;Keywords: alternative splicing; peptidyl-dipeptide hydrolase; transmembrane
peptidy1-dipeptidase A (EC 3.4.15.1) precursor - mouse N;Alternate names: ACE; angiotensin-converting enzyme; carboxycathepsin; dipeptidy1 c.().Species: Mus musculus (house mouse) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A34171; A29220; A61477 R;Bernstein, K.E.; Martin, B.M.; Edwards, A.S.; Bernstein, E.A. J. Biol. Chem. 264, 11945-11951, 1989 A;Title: Mouse angiotensin-converting enzyme is a protein composed of two homologous A;Reference number: A34171; MUID:89308599; pMID:2545691 A;Accession: A34171; MUID:89308599; pMID:2545691
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                                                                                                                                                                                                                                                                                                                                                                        596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 TDEAKADRFVEEYDRTAQVLLNEYAEANWQYNTNITIEGSKILLEKSTEVSNHTLKYGTR 128
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                                                                                                                                                                                                                                                                                                                                                                           MKLGYSKPWPEAMKLITGOPNMSASAMMNYFKPLTEWLVTENRRHGETLGWPEYNWAP 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FDPGSKFHVPANVPYVRYFVSFIIQFQFHEALCRAAGHTGPLHKCDIYQSKEAGKLLADA 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETY 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIQYFMQYKDLPVTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLPNWTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG
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A;Molecule type: mRNA
A;Residues: 1-1312 <BER>
A;Residues: 1-1312 <BER>
A;Cross-references: GB::U04947
R;Bernstein, K.E.; Martin, B.M.; Bernstein, E.A.; Linton, J.; Striker, L.;
R;Bernstein, K.E.; Martin, B.M.; Bernstein, E.A.; Linton, J.; Striker, L.;
J. Biol. Chem. 263, 11021-11024, 1988
A;Title: The isolation of angiotensin-converting enzyme cDNA.
A;Reference number: A29220; MUID:88298730; PMID:2841312

Striker,

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A;Accession: A29220
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-332 <BE2>
A;Cross references: GB:J03940; NID:g191583; PIDN:AAA37146.1; PID:g191584
A;Cross references: GB:J03940; NID:g191583; PIDN:AAA37146.1;
A;Cross references: GB:J0
                                          N;Alternate names: angiotensin converting enzyme C;Species: Gallus gallus (chicken)
C;Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 28-May-1999
C;Accession: JC2489
R;Esther, C.R.; Thomas Jr., K.E.; Bernstein, K.E.
Biochem. Biophys. Res. Commun. 205, 1916-1921, 1994
                                                                                                                                                                                                                                      peptidyl-dipeptidase A (EC 3.4.15.1) - chicken N;Alternate names: anoiotenein communication --
               Biochem. Biophys. Res. Comr
A; Title: Chicken lacks the
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A; Molecule type: mRNA
A; Residues: 1-1193 <EST>
A; Residues: 1-1193 <EST>
A; Residues: GB:140175; NID:9685168; PIDN:AAA75554.1; PID:g994708
A; Cross-references: GB:140175; NID:9685168; PIDN:AAA75554.1; PID:g994708
C; Comment: This enzyme is a zinc dependant dipeptidyl carboxypeptidase the c; Superfamily: mammalian peptidyl-dipeptidase A
C; Superfamily: mammalian peptidyl-dipeptide hydrolase; zinc
C; Keywords: metal binding; peptidyl-dipeptide hydrolase; zinc
C; Keywords: metal binding site: zinc, catalytic (Glu, His, Glu, His) #sta
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                                              ADQSIKVRISLKSALG------DKAYEWNDNEMYLFRSSVAYAMRQYFLKVK
                                                                                               AMKLGFSKPWPEAMQLITGQPNMSAEALMSYFEPLMTWLVKKNTENGEVLGWPEYSWTPY
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                                                                                                                                             MLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWL--KDQNKNSFVGW-STDWSPY
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C;Accession: JC2038

R;Koike, G.; Krieger, J.E.; Jacob, H.J.; Mukoyama, M.; Pratt, R.E.; Dzau, V.J.

Biochem. Biophys. Res. Commun. 198, 380-386, 1994

A;Title: Angiotensin converting enzyme and genetic hypertension: Cloning of rat cDNAs A;Reference number: JC2038; MUID:94121658; PMID:8292044

A;Accession: JC2038

A; Molecule type: m: A; Residues: 1-1313

mRNA

<KOI>

peptidyl-dipeptidase A (EC 3.4.15.1) - rat
N;Alternate names: angiotensin converting enzyme; kininase II
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 *sequence_revision 10-Sep-1999 *text_change 10-Sep-1999

con

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peptidy1-dipeptidase A (EC 3.4.15.1) precursor, testicular - rabbit
N;Alternate names: angiotensin I-converting enzyme; dipeptidy1 carboxypeptidase I; por C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Bete: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A34402; A60724; A36232; C18700
R;Kumar, R.S.; Kusari, J.; Roy, S.N.; Soffer, R.L.; Sen, G.C.
J. Biol. Chem. 264, 16754-16758, 1989
A;Tille: Structure of testicular angiotensin-converting enzyme. A segmental mosaic is A;Reference number: A34402; MUID:89380303; PMID:2550457
A;Rocession: A34402
A;Molecule type: mRNA
A;Residues: 1-737 <KUM>
A;Residues: 1-737 <KUM>
A;Residues: 1-737 <KUM>
A;Residues: Dharmacol. 16(Suppl.4); S14-S18, 1990
A;Title: Angiotensin-coverting enzyme: structural relationship of the testicular and A;Reference number: A60724; MUID:91155372; PMID:1705622
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A;Note: the authors translated the codon ACC for residue 159 as Tyr
C;Comment: This enzyme is a zinc-containg dicarboxy peptidase that cleaves angiotensin C;Comment: This enzyme plays a critical role in blood pressure homeostasis and is the t C;Superfamily: mammalian peptidyl-dipeptidase A C;Keywords: alternative splicing; peptidyldipeptide hydrolase; transmembrane protein; z F;393-400,990-999/Region: catalytic #status predicted
F;1264-1284/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIBEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKLGYSKQWPEAMKIITGQPNMSASAIMNYFKPLTEWLVTENRRHGETLGWPEYTWTP 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIQYFMQYKDLPVTFREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSE-GSGYEHDIN 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDSWRSSYESDDLE------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKTFDVSNFQNSTIKRIIKKVQNVDRAVLPPNELEEYNQILLDMETTYSVANVCYTNG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TDEAKANRFVEEYDRTAKVLWNEYAEANWHYNTNITIEGSKILLQKNKEVSNHTLKYGTW 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDPGSKFHVPANVPYIRYFISFIIQFQFHEALCRAAGHTGPLYKCDIYQSKEAGKLLADA 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLMKMALDKIAFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGD 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETY 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTSVNMEELVIAHHEMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGCLPAHLLGDMWGREWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCLSLEPDLTNIMATSRKYEELLWVWKSWRDKVGRAILPFFPKYVDFSNKIAKLNGYSDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; DB 1;
4.7e-82;
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A; Residues: 154-160; 236-242 < CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A3623
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                                   WPQYTWTPNSARS
                                                                        W-STDWSPYADQS 617
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A; Accession: A60724
A; Status: translation not shown
A; Molecule type: mrNA
A; Molecule type: mrNA
A; Residues: 73-173 <SEN>
A; Note: identical sequences were obtained for mrNAs from lung
R; Chen, Y. N.P.; Riordan, J.F.
Biochemistry 29, 10493-10498, 1990
A; Title: Identification of essential tyrosine and lysine resid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Iwata, K.; Lai, C.Y.; El-Dorry, H.A.; Soffer, R.L. Biochem. Biophys. Res. Commun. 107, 1097-1103, 1982 A;Title: The NH2-and COOH-terminal sequences of the angiotensin-converting A;Reference number: A90107; MUID:83048249; PMID:6291514 A;Accession: C18700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Rosidues: 33-35, 'SN', 38-39, 'SS'; 'FAEL', 737 <IWA>
A;Rosidues: 33-35, 'SN', 38-39, 'SS'; 'FAEL', 737 <IWA>
A;Note: several of the amino acids in reported are tentative
C;Comment: The pulmonary and testicular isoforms of this enzyme differ substantially
ggests that the two isoforms arise by alternative splicing of one gene.
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: alternative splicing; peptidyldipeptide hydrolase; testis; transmembrane
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                                                                                                                                      CPPAPRSQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCKAAGHTGPLHTCDIYQS
                                                                                                                                                                            VEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AARLNGYVDAGDSWRSMYETPTLE------QDLERLFQELQPLYLNLHAYVGRALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANVCRVDG--SCLQLEPDLTNLMATSRKYDELLWVWTSWRDKVGRAILPYFPKYVEFTNK
KEAGKRLADAMKLGYSKPWPEAMKVITGQPNMSASAMMNYFKPLMDWLLTENGRHGEKLG
                                                           TEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQN--KNSFVG
                                                                                                                                                                                                                                                                                                                                    FQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGV
                                                                                                                                                                                                                                                                                                                                                                                                              DLVVVHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSINLLSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEADKFF ISLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNME
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                                                                                                                                                                                                                                                                        -GGGYEHDINFLMKMALDKIAFIPFSYLVDEWRWRVFDGSITKENYNQEWWSLRLKYQGL
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Pred. No. 1.4e-80;
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A; Residues: 34-55 < KIR>
C:Comment: This enzyme converts angiotensin I to angiotensin II in presence of ver, the enzyme has been found in renal tubules and intestinal mucosa. C:Superfamily: mammalian peptidyl-dipeptidase A
C:Keywords: alternative splicing: blood pressure control; chloride; glycoprotei F;1-33/Domain: signal sequence #status predicted <SIG> F;34-1309/Product: peptidyl-dipeptidase A, pulmonary #status experimental <MATP F;59,79,150,322,448,512,680,698,717,945,1194/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R:Kumar, R.S.; Thekkumkara, T.J.; Sen, G.C.

J. Biol. Chem. 266, 3854-3862, 1991

A:Title: The mRNAs encoding the two angiotensin-converting
A:Reference number: A38655; MUID:91139683; PMID:1847388
A:Accession: A38655
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A; Residues: 34-44; 754-755, 'L', 757 <IW2>
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S35484; A23455, A18700; A38655; A49726; S17509
R;Thekkumkara, T.J.; Livingston III, W.; Kumar, R.S.; Sen, G.C.
Nucleic Acids Res. 20, 683-687, 1992
A;Title: Use of alternative polyadenylation sites for tissue-specific transcription
A;Reference number: S35484; MUID:92178960; PMID:1311831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: The Mg(2+)-ATPase of rabbit skeletal-muscle transverse tubule A; Reference number: S17509; MUID:91378880; PMID:1654880 A; Accession: S17509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Kirley, T.L.
Biochem. J. 278,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein A; Residues: 1236-1258 < RAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M58579
R;Ramchandran, R.; Sen, G.C.; Misono, K.; Sen, I.
J. Biol. Chem. 269, 2125-2130, 1994
A;Title: Regulated cleavage-secretion of the membrane-bound angiotensin-converting enzyma;Reference number: A49726; MUID:94124568; PMID:8294466
A;Accession: A49726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-88 < KUM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 34-47, 'N', 49-55 < IWA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-1309 <THE>
A; Cross-references: EMBL: X62551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptidyl-dipeptidase A (EC 3.4.15.1) precursor, pulmonary splice form - rabbit N.Alternate names: angiotensin-converting enzyme; dipeptidyl carboxypeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A23455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
                                                                     647
         70
                                                                                                                                                                                                                        POCGI
SAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYST
                                                              TDEAEASRFVEEYDRSFQAVWNEYAEANWNYNTNITTEASKILLQKNMQIANHTLIYGNW 706
                                                                                                                       TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----
                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                  29.9%;
                                                                                                                                                                                                                  Score 1283; DB 1;
Pred. No. 3.4e-80;
                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                                                                                                               glycoprotein;
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Matches

Local Similarity

Conservative

108;

Mismatches No.

246;

Indels

22;

Gaps

7;

Pred.

3.8e-65;

8 LLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGD

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Eur. J. Blochem. 237, 414-423, 1996
A;Title: Cloning and characterisation of angiotensin converting enzyme from A;Feference number: $65431; MUID:96215437; PMID:8647080
A;Accession: $65472
A;Molecule type: DNA
A;Residues: 1-611 <WIJ>
A;Rosidues: 1-611 <WIJ>
A;Cross-references: EMBL:143965; NID:9908759; PIDN:AAA70427.1; PID:9908760
A;Note: the source is designated as Haematobia irritans exigua
A;Accession: $65431
A;Molecule type: protein
A;Residues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <WIW>
A;Rosidues: 18, P', 20-42;75-77, 'Q', 79-81, 'X', 83-84;179-190 <W
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N;Alternate names: angiotensin I-converting enzyme
C;Species: Haematobia irritans (horn fly)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 22-Jun-1999
C;Accession: S65472; S65431
R;Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.;
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24.7%;
                                 Score 1058;
                                 DB 2;
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peptidyl-dipeptidase A (EC 3.4.15.1) 67k precursor - fruit fly (Drosophila melanogaster N;Alternate names: angiotensin-converting enzyme C;Species: Drosophila melanogaster C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 26-Feb-1998 C;Accession: A57533
C;Accession: A57533
A;Title: Cloning and expression of an evolutionary conserved single-domain angiotensin A;Reference number: A57533; MUID:95293950; PMID:7775412
A;Accession: A5753
A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-615 CCOR> A;Cross-references: GB:U25344
C;Genetics:
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C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: peptidyldipeptide hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLG-KGDFRILMCTK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTQDQFFTVHHEMGHIQYFLQYQHQPFVYRTGANPGFHEAVGDVLSLSVSTPKHLERVGL
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                                          KWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSGIEPPVVRTEKDFDAPAKYHVSADVEYLRYLVSFIIQFQFYKSACITAGEYVPNQTEY 535
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                ELAKFMKEVASDTTKFQWRSYQSEDLKRQFKALTKLGYAALPEDDYAELLDTLSAMESNF
                                                                                                                                                   LLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGD
                                                                                                      LLATLAVTQALVKEEIQAKEYLENLNKELAKRTNVETEAAWAYGSNITDENEKKKNEISA 67
                                                                                                                                                                                                Conservative
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35.8%; Pred. No. 7.86
tive 120; Mismatches
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nes 251;
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C;Species: Drosophila melanogaster
C;Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jul-2000
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C;Superfamily: mammalian peptidyl-dipeptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Taylor, C.A.M.; Coates, D.; Shirras, A.D. Gene 181, 191-197, 1996
A;Title: The Acer gene of Drosophila codes A;Reference number: JC5374; MUID:97128790;
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A; Residues: 1-630 <TAY>
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                                                                                                                                                                                                                                               16 WLPHGLSMGNSCSASVLE-ARRFFELENEQLRRRFHEEFLSGYNYNTNVTEANRQAMIEV
                                                                                                                                                                                                                                                                                     6 WILLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNA 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KMFQMGDDFFTSMNLTKLPQDFWDKSIIEKPTDGRDLVCHASAWDFYLIDDVRIKQCTRV
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                                                                                                      IYSTGKVCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYV 184
                VLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYV
                                                                NYATATVCSYTNRSDCSLTLEPHIQERLSHSRDPAELAWYWREWHDKSGTPMRQNFAEYV 194
                                                                                                                                                       YARNAELNKRLAQQIKSSDYVQSEDADIRRQAEHLSKLGASALNADDYLALQNAISSMQT 134
                                                                                                                                                                                                {\tt GDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMST}
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                                                                                                                                                                                                                                                                                                                                       Conservative 113; Mismatches
                                                                                                                                                                                                                                                                                                                                                               24.0%; Score 1030; DB 2; 35.6%; Pred. No. 3.4e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for an angiotensin-converting enzyme homo PMID:8973330
                                                                                                                                                                                                                                                                                                                                                                                      Length 630;
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715792
715792
hypothetical protein C42D8.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Accession: T15792
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A:Introns: 140/3; 170/3; 194/3; 300/2; 467/3; 551/2; 600/2; 697/3; 774/2; 851/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U56966; NID:g1293844; PID:g1293847; PIDN:AAA98719.1; GSPDB:GNOCA;Experimental source: strain Bristol N2; clone C42D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: T15792
A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
A;Residues: 1-907 <HAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Hallsworth, K.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid C42D8
A;Reference number: Z18405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP:C42D8.5
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241 HAYVRAKLMNAY--PSYTSPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMV 298
                                                 337 NIITISNEGAKLNGFANGGAMWRSAFDMSSKVHKAEF---DLNKQIDKIYSTIQPFYQLL
                                                                                                                                                                                                    122 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 181
                                                                                                                                                                                                                                                   218 LDEAENVLTMFVRSTSMQAKQFDMASVTDEKVMRQLGYVSFEGMSALAPSRFADYSQAQA 277
                                                                                                                                                                                                                                                                                                                                                                   160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543 LTLDNCDIFGSKAAGRSLSQFLSKGNSRHWKEVLEEFTGETEMDPAALLEYFEPLYQWLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               603 QE--NSRLGVPLGWGP 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              597 DQNKNSFVGWSTDWSP 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                EYYVLKNEMARANHYEDYGDYWRGDYEVNG-VDGYDYSRGQLIEDVEHTFEEIKPLYEHL 240
                                                                                                                                                       ALNRDSKDSTICDKDVPPPCALQKIDMDSIFRNEKDASRLQHLWVSYVTAIAKS-KPSYN
                                                                                                                                                                                                                                                                                                                                                      SSNYWKTDNLQAPGSIKD--EEKLRSWLAGYEAEAIKVLREVALSGWRYFNDASPSLKLA 217
                                                                                                                                                                                                                                                                                                                                                                                                     SSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQN 61
                                                                                                                                                                                                                                                                                                       MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 12:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVDSHYFYVVHHELGHIQYYLQYEQQPAVYRGAPNPGFHEAVGDVIALSVMSAKHLKAIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFGGVEPPVFRTEKDFDPPAKYHIDADVEYLRYFAAHIFQFQFHKVLCRKAGQYAPNNSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --LHKCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLK 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIE-NGRLDEKSRINQLEKQALSKIVFLPFGYAVDKYRYAVFRNELDESQWNCGFWQMRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.0%; Score 642.5; DB 2; 27.0%; Pred. No. 3.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       289;
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A;Molecule type: DNA
A;Residues: 1-532 <STO>
A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB04090.1; GSPDB:G
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
A; Gene: BHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein BH0371 [imported] - Bacillus halodurans (strain C-125) C:Species: Bacillus halodurans C:Species: D1-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
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       297 MVDQAWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQK-AVCHPTAWDLGKGD 355
                                                            212 KDEIDEERAKVLKIKKDDLRP------250
                                                                                                             245 -----RAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQK-PNIDVTDA 296
                                                                                                                                                                                                              188 NEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHT----FEEIKPLYEHLHAYV 244
                                                                                                                                                                                                                                                                119 NGSRVSNNE------LLDTLRYDLDHERRKQAWFA-SKEVGKRTEKDLLQLIRKR 166
                                                                                                                                                                         167 NEVARNLGFETF-
                                                                                                                                                                                                                                                                                                                 128 STGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             631 KLNDRWWEIRNKYEGVRSPQPYNTSNLD--ALIHNSVSQVHS----PATRTLISYVLKFQI 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  583 PLLNYFEPLFTWLKDQNK--NSFVGWSTDWSPYADQSI 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               686 LKALCQRELFWLSEG----CILSEDTT--EKLRETMKLGSSITWLKALEMISGKGELDAQ 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511 PNDFRVKACAQLGEPDFEQAHSLLVQTYYQYLYKDQSLLFREQASPVITDAIANAFAHLS 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 EEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-NVQNMNNAGDKWSAFLKEQS--- 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EQDIERFLSEQNKRVEDLYQPVLLNHWMVATTGEQEWSDKHEQSLSEYWAHFSDRESFQK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                              VTRFRKIDSLPLMQRRQLDDLHDKMIKNQFE--EGTRQQILSLE--KKISHVFTTFQPQV 118
                                                                                                                                                                                                                                                                                                                                                                                                                  -----TLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLLEYYEPLINWLRNTNEIDQVVVGWDGEGTPFTVEEI 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QWMKKWWEMKREIVGVVEPVPHDETYCDPASLFH--VSNDYSFIRYYTRTL----YQFQF 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNPHYLYSQKLVPSEHLDIKDSVIINKLYKESLESFTKLPFTIAADNWRYELFDGTVPKN 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGDFRILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAFNTQNYTTKKMEVTAYRYFKSAGFPHLPKSYWTSSIFARVWS-KDMICHPAAALDMRA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D----QAWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHP-TAWDL-G 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83; Mismatches 213; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 157; DB 2;
Pred. No. 0.0058;
                                                                                                                                                               YHMSFATQELDLEQTFAMFETIKKSSDQAFRMI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
```

Length 532;

Gaps

Qy 118 TILNTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLR 177 :: :: : : : : : : : : : :	Query Match Query Match 3.6%; Score 154; DB 2; Length 502; Best Local Similarity 20.1%; pred. no. 0.0086; Matches 128; Conservative 101; Mismatches 215; Indels 192; Gaps 35; Qy 20 TIEEDARTFLDKFNHEAEDLFYQSSLASWNUTNITEENVQNMNNA 65	AFI310 probable thermostable carboxypeptidases homolog lmol886 [imported] - Listeria monocytogenes C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C;Accession: AF1310 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D; Jones, L. M.; Karst, U. Science 294, 849-852, 2001 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Accession: AF1310 A;Residues: 1-502 cGLA> A;Cross-references: GB:NC_003210; PIDN:CAC99964.1; PID:gl6411339; GSPDB:GN00177 A;Experimental source: strain EGD-e C;Genetics: A;Gene: Imo1886 C;Superfamily: Thermus aquaticus carboxypeptidase Taq	Qy 356 FRILMCTKVTMDDFLTAHHEMGH-IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAAT 414 [::::::::::::::::::::::::::::::::::
Oy 120 LNTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLMAWESWRSEVGKOLRPL 179 :: : : : : : : : : : : :	Query Match Query Match 3.4%; Score 147; DB 2; Length 502; Best Local Similarity 19.4%; Pred. No. 0.026; Matches 124; Conservative 95; Mismatches 223; Indels 196; Gaps 33; Qy 20 TIEEQAKTFLDKENHEAEDLFYOSSLASWNYNT	RESULT 16 AE1682 probable thermostable carboxypeptidases homolog lin1999 [imported] - Listeria innocua C;Species: Listeria innocua C;Species: Listeria innocua C;Date: 27-Nov-2001 frequence_revision 27-Nov-2001 ftext_change 14-Dec-2001 C;Accession: AE1682 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Accession: AE1682 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-502 <gla> A;Experimental source: strain Clip11262 C;Genetics: A;Gene: lin1999 C;Superfamily: Thermus aquaticus carboxypeptidase Taq</gla>	Qy 406 -EIMSLSAATPKHLKSIGLLSPDEQEDNETEINELLKQALTIVGTLP- 451

Qy	Оу	Qу	Qу	ОУ	ОУ	Оy	Qy Db	Que Bes Mat	A; Res A; Res A; Res A; Crc A; Crc A; Gen	R; Kar Naka DNA F A; Tit	RESULT AI2011 peptid C; Spec A; Note C; Date C; Acce	Db Qy	Db Qy	Db 04	Db Qy	Db
425	365 : 419 :	319 360 I	275 I 305 I		158 220	112 160	52 106	Query Match Best Local Matches 11	rerencession tus: lecule lecule idues sidues sidues lecime letics le: al	leko, Izaki, Res. 8	IT 17 [1] [de sy cies: cies: No ce: No ces: 14	563 466	507 410	451 356	404 302	246
SPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREI 484	TMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLL 424 : : : : : : : : : : : : : : :	GLPNWTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKV 364 :	WTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV- 318 	SRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRF 274 : : ::	YNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDY 217 :: :	KSKRLNTILNTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLD 157	TNITEENVQNMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSYLSED 111 : : : : : : : : :	y Match 3.3%; Score 139.5; DB 2; Length 987; Local Similarity 19.6%; Pred. No. 0.24; hes 117; Conservative 80; Mismatches 208; Indels 191; Gaps 26;	D:21595285; PMID:11759840 ; PIDN:BAB78013.1; PID:g17135467; CC 7120	.P.; K , M.; of the	RESULT 17 AIJ011 AIJ011 peptide synthetase [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AIZ011	SEPWTLALENVVGAKNMNVRPLLNVFEPLFTWLKDQNK 600 :: : :: TKKPLEILTDTTG-EGLNPTYLLDLLEKRYAYVYQFNK 502	SNDYSFIRYYTRTL-YQFQFQEALCQAAKHEGPLHKCDISNSTBAGQKLFNMLRLGK 562 	PFTYMLEKWRWMYFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHV 506	VGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLLKQALTIVGTL 450 : :: : : : : : : : : : : :	ITTRYNENDFKMAVFGTIHEGGHAIYEQNFDAALVGTPLANGASNGIHESQSLFYE 301

Оy	463 AVDYGEGQKRLV
ДЬ	495UNIP
Qy	545SNSTEAGQKLENMLRLCKSEPWTLALENVVGAKNMNVRPLLNYFEPLETWL
Db	
RESULT B82938 zinc me	UT 18 38 metalloproteinase oligoendopeptidase F UU065 [imported] - Ureaplasma urealyticum
C;Species: C;Date: 18- C;Accession	Ureaplasma urealyticum Aug-2000 #sequence_revision 20-Aug-2000 . B82938
R;Glass,	R;Glass, J.S.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, submitted to GenRank February 2000
A; Des	A; Description: The complete sequence of Ureaplasma urealyticum: A; Reference number: A82870
A; Acc A; Sta A; Mol	A;Accession: B82938 A;Status: preliminary A;Molecule type: DNA
A; Res A; Cro	A;Residues: 1-608 (GLA> A;Residues: 1-608 (GLA> A;Cross-references: GB:AE002106; GB:AF222894; NID:g6899011; A;Experimental source: serovar 3; biovar 1
** ** *	Gene: pepr-1; UU065 Genetic code: SGC3
Query Best I Matche	Query Match 3.2%; Score 139; DB 2; Length 608 Best Local Similarity 19.1%; Pred. No. 0.13; Matches 132; Conservative 93; Mismatches 226; Indels
Qy Db	22 EEQAKTFLDKFNHEABDLFYQSSLASWNYNTNITEENVQNMN
Qy	64 NAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSV-
DЬ	79PKWNSWSQKLSASFYELETALSNYNSVVLANEAKIKEYLTDSQLNYYTRKYNEIF
Qy	108GKVCNPDNPQECLL
Db	134 RYQPHTLNNEQSKLFSTLIRADEGFSTIFSTYTNNDMKFSDAIDAKGKKHPIKNEAEAFY
Qy	VLKNE
Дb	194 HLKSKDRVLRKSA-YLSMYRAYYDSRESITKMLYYNYLSL-NQQAKAKNFDDY-
Qy	204 RGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLP
Дb	247 KAAEDDVVDKSLITLIYDQVKLYKDTNEDYKKVRNTYLKKLIKVSKIED-
Qy	264 AHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLPNM
Вb	296WDNGLPLISKKIDIPIEEAK-QMAIDSLSILGDEYVS-
Qy	324 TQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGHIQYDM
Ъ	334 KRAFDEKWYSWLPQKGKRGGAYSIGGTKGISKYYILMNYTNSLRDVQTIVHELGHSMHS-
Qy	384 AYAAQPFLLRNGANEGFHEAVGEINSLSAATPKHLKSIGLLSPDFQEDNETEINFL-
ф	393NEVYKIFYAEIASISNEVYLNYYL
Qy	440GEIPKDQMMKKWWE
Db	426 LEKYKNDLEMKLMILDEMISGFFATTTRQVIFSNFEWIANELINSGAPFTADVVMKEVQK
Qγ	480 MKREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQF

Qy 535 HEGPLHKCDI-SNSTEAGQKLFNMLRLGKS-EPWTLALENVVGAKNMNVRPLLNYFEPLF 592	AYLEINHDYTGYKYNKNKISKYDEANALILINIPHFYTGNFYVYKYVIGQIC	A 97 WYEDYDEDER	QY 428 FQEDNETEINFLKQALTIVGTLPFTYMLEKWBWMVFKGEIPKDQWMKKWWEMK-REIVG 486 :: : : : : : : : : : Db 432 YENDDLMRLYILDEMISGFIATTTRQAIFSNFEWVANEWINQGEEFSWNKIVL 484	Qy 368 DFLTAHHEMGHIQYDMAYAAQDFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPD 427	Qy 308 FKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMD 367	Qy 249 MNAXPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAM-VDQAWDAQRI 307 : : : : : : : : :	Qy 191 ARANHYEDYGDYWRGDYEVNGVDGYDXSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKL 248 : ::::	Qy 131 KVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEM 190	Qy 95YSTG 130 125 LIKYQLEYEELWRYEKHILNEQQQKVYTAISRFSSSFGDIFDYLLDSDMQYQDGINYKKQ 184	Qy 49 NYNTNITEENVQNMNNAGDKWSAFLK-EQSTLAQMYPLQEIQNLTVK 94	Query Match 3.2%; Score 136; DB 2; Length 611; Best Local Similarity 19.5%; Pred. No. 0.2; Matches 119; Conservative 100; Mismatches 256; Indels 134; Gaps 27;	A;Gene: pepF-2; UU521 A;Genetic code: SGC3	0 0 74 14	zinc metalloproteinase oligoendopeptidase F UU521 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Bate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C;Accession: DB2881	Qy 567 TLALENVVGAKNMVRPLLNYFEPLFTWLKD 597	Qy 524 QFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLGKSEPW 566 :	Db 486 LELEYTNKPIVEDLNSIYSLSSITPLRIPHFYVGNEYVYKY 526
Qy 540 HKCDISNSTEAGQKLFNMLRL-GKSEPWTLALENVVGAKNMNVRPLLNY 587	TPQTDAEGILQDVHWAGGDFGYFPSYALGYNYAAQLKOKMLEDLPEFDALLERGEF	Ov A87 VVEDUDHDEMYCDDAGIEHVGNDYS-ETRYYBRTIYOFOFOEAICOAAKHEGPL 539	Qy 429 QEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVG 486 : ::: : :: : : : :: ::: ::::: ::::::	QY 386 AAQPFLIRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDF- 428	Qy 332 MLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGHIQYDMAY 385	QY 279 YSLTVPFGOKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLPNMTQGFWENS 331	QY 219 RGQLIEDVEHTFEEBIKPLYEHLHAYVRAKIMNAYPSYISPIGCLPAHLLGDMWGRFWTNL 278	Qy 180 YEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYS 218 - - - -	Query Match 3.1%; Score 135; DB 2; Length 501; Best Local Similarity 20.9%; Pred. No. 0.18; Matches 98; Conservative 65; Mismatches 164; Indels 142; Gaps 26;	C;Genetics: A;Gene: ypwA C;Superfamily: Thermus aquaticus carboxypeptidase Taq	A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-501 < KUN> A; Residues: 1-501 < KUN> A; Cross-references: GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB14125.1; PID:g26346 A; Experimental source: strain 168 A; Experimental source: strain 168	A;ILLE: IIE complete genome sequence of the politic sequence of the politic sequence A;Reference number: A69580; MUID:98044033; PMID:9384377 A;Accession: D69943 A. Status: numbiginary: nucleic acid sequence not shown: translation not shown	y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.	R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997	RESULT 20 D69943 Carboxypeptidase homolog ypwA - Bacillus subtilis C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000	Qy 593 -TWLKDQNK 600 : : Db 592 NSWIDDYIK 600	Db 537GLINAIRIFNNKANAKEKYFCFFKSGGSLSPLETINILDIK-INENDWEEVNIIF 591

Db 451 HPIK------QWLTEKVHIHGKRKKPLDIIKDATG-EELNVRYLIDY 490

Search completed: March 13, 2003, 16:58:59 Job time: 33 secs

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1 MSSSSWLLLSLVAVTAAQST.....ISKGENNPGFQNTDDVQTSF 805
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 SwissProt_40:*
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NEBU_HUMAN
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p010751 gallus gall
p47820 rattus norv
p12822 oryctolagus
p22968 oryctolagus
p10714 drosophila
p10715 haematobia
p50848 bacillus su
p39118 bacillus su
p39118 staphylococ
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106.5 106.5 105.5 105.5 104.5 104.5 104 103.5 103.5 103.5 103.5
1312 1279 645 1002 757 639 834 569 511 1162 660 704
RA50_YEAST BCHL_CHLVI REP_BUCAI POL_HV1U4 RTS1_YEAST GLGB_BACST GLGB_BACST CASL_HUMAN CYSP_PLAFA CTAQ_THEAQ BXEN_CLOBU MM02_HUMAN GLGB_YEAST
p12753 saccharomyc o50314 chlorobium p57654 buchnera ap p24740 human immun p38903 saccharomyc p38903 saccharomyc p30538 bacillus st Q14511 homo sapien p25805 plasmodium p42663 thermus aqu q06366 clostridium p08253 homo sapien p32775 saccharomyc

ALIGNMENTS

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-!- TISSUE SPECIFICITY OF THOUGHT TO	somatic (AC P12821); are produced by discission of the sound of the so	-!- SUBCELLULAR LOCATION	-!- COFACTOR: BINDS I ZINC IOW.			BRADYKININ, A POTENT VASCULLATATOR.	VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN. ALSO REFERENCE	-	Biochem	somatic and testis isozymes.";	Ehlers M.R., Riordan J.F.;	ZINC-BINDING. MEDLINE=91308093; PubMed=1649623;	[4]	Nat. Genet. 22:59-62(1999).	Rieder M.J., Taylor S.L., Clark A.S., "Formal Converting enzyme.";	580; PubMed=10319862; Nickerson D.A.;	[3] SECTION OF EROM N.A., AND VARIANTS P-32; G-49 AND S-712.	FEBS Lett. 252:99-104(1989).	lar transcript of the angloceusin i compared the enzyments.	Alhenc-Gelas F.;	MEDLINE=89338720; PubMed=2547055, Allegrini J., Hubert C., Corvol P.,	SEQUENCE FROM N.A	Proc. Natl. Acad. SC1. U.S.A. 00://31	iotensi	to the	cular angiotensin-convert	UENCE FROM N.A. LINE=90045671; PubMed=2554286;	NCB1_Tax+P-7000	Primates;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eucereoscom; Eukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo.		Angiotensin-converting engine, in a special carboxypeptidase I) (Kininase II).	isoform precursor	(Rel. 19, Created)	HUMAN STANDARD;	

REGULATION BY ANDROGENS

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243 YVRAKLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 301
                         231 YVELINQAARLNGYVDAGDSWRSMYETPSLE-----QDLERLFQELQPLYLNLHA
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                                                                                                                                                                            61 TSAOSPHLVTDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTHITTETSKILLQKNNQIA 120
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PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
Glycoprotein; Transmembrane; Testis; Signal; Alternative splicing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMML outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                 YVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHA 242
                                                                                                  MSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEE 182
                                                                           METTYSVATVCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPK 230
                                                                                                                            NHT-----LKYGTQARKEDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLD 172
                                                                                                                                                   NNAGDKWSAFLKEOSTLAOMYPLQEIONLTVKLQLQALQQNGSSVLSEDKSKRLNTILNT 122
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A33979; A33979.
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41.8%; Pred. No. 1.
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(BY SIMILARITY)
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"Angiotensin-converting enzyme: zinc- and inhibitor-binding stoichiometries of the somatic and testis isozymes."; Biochemistry 30:7118-7126(1991).
                                                        Ehlers M.R., Riordan J.F.
                                                                  MEDLINE=91308093; PubMed=1649623;
                                                                                                                     performance liquid chromatography: properties and N-terminal amino acid sequence. ^{"};
                                                                                                                                                   "Purification of human lung angiotensin-converting enzyme by high-
                                                                                                                                                                                Takeuchi K., Shimizu T., Ohishi N., Seyama Y., Takaku F.,
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND VARIANTS S-261; W-561 AND S-1286. MEDLINE-99251580; PubMed-10319862; Rieder M.J., Taylor S.L., Clark A.G., Nickerson D.A.; "Sequence variation in the human angiotensin converting enzyme.";
                                                                                              ZINC-BINDING
                                                                                                                                                                                                         MEDLINE=90110025; PubMed=2558109;
                                                                                                                                                                                                                                TISSUE-Lung
                                                                                                                  f. Biochem. 106:442-445(1989).
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                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 85:9386-9390(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
CACE) (Dipeptidyl carboxypeptidase I) (Kininase II) (CD143 antigen).
                                                                                                                                                                                                                                                                                                                                                                               "Two putative active centers in human angiotensin I-converting enzyme
                                                                                                                                                                                                                                                                                                                                                                                                    Soubrier F., Alhenc-Gelas F., Hubert C., Allegrini J., John M.,
Tregear G., Corbol P.;
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Mammalia; Eutheria; Primates; Catarrhini;
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PIR; PQ0004; PQ0004.
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InterPro; IPR000130; Zn_MTpeptdse.
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proSITE; pS00142; ZINC_pROTEASE; 2
                                                                                                      CARBOHYD
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                                     CARBOHYD
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CATALTYTC ACTIVITY: Release of a C-terminal dipeptide, oligopeptide-[-xaa-xbb, when xaa is not Pro, and Xbb is neither algopeptide-[-xaa-xbb, when xaa is not Pro, and Xbb is neither asp nor Glu. Converts angiotensin I to angiotensin II. COTACTOR: BINDS 2 ZINC IONS.

SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 isoforms; somatic (shown here) and testis-specific (AC P22966); are produced by alternative splicing. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.

DATABASE: NAME-PROW; NOTE-CD guide CD143 entry; www-"http://www.nobi.nlm.nih.gov/prow/cd/cdi43.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE VASCOONSTRICTOR ACTIVITY OF ANGIOTENSIN. ALSO ABLE TO INACTIVATE
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ZINC 2 (CATALYTIC)
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INC 2 (CATALYTIC) (BY
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                                                               1163
                                                                                                                                  1103
                                                                                                                                                                                               1044 SD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 1102
1223 QYNWTPNSARS 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   698 --LKYGTQARKEDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   644 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT-----
                                                                                                                                                                                                                                                                                                                                                                                                  864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     814
                                                                                                                                                                                                                                  430
                                                                                                                                                                                                                                                                984 VVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGG 1043
                                                                                                                                                                                                                                                                                                   370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 FLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNMNNAGDKWSA 71
                                                                                                                                                                                                                                                                                                                                                               AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLNGYVDAGDSWRSMYETPSLE------QDLERLFQELQPLYLNLHAYVRRALHRH 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYYVLKNEMA 19:
                                                                                                                                                                                                                                                                                                LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 429
                                                                                                                                                                                                                                                                                                                                 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL 983
                                                                                                                                                                                                                                                                                                                                                                                                                                Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VCHPNG---SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA
                                                                                                                                                                                                                                                                                                                                                                                                YGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 923
                                                                                                                              PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 1162
                             STDWSPYADQS 617
                                                             AGORLATAMKLGFSRPWPEAMOLITGOPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 1222
                                                                                             AGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW- 606
                                                                                                                                                            PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE
                                                                                                                                                                                                                               EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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42
1306 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1337; DB 1;
Pred. No. 9.4e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR_011708
R -> S.
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D -> R (IN REF. 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
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RESULT 3
ACET_MOUSE STANDARD; PRT; 732 AA.

ID ACET_MOUSE STANDARD; PRT; 732 AA.

AC P22967;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiotensin-converting enzyme, testis-specific isoform precursor
DE (EC 3.4.15.1) (ACE-T) (Dipeptidyl carboxypeptidase I) (Kininase I
GN DCP1 OR ACE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammaila; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
RP SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0791; PEPDIPTASEA.

PRINTS; PRO04184; Peptidase_M2; 1.

PRODOM; PD004184; Peptidase_M2; 1.

PROSITE; PS00142; ZINC_PROTEASE; 1.

Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase; Hydrolase; Metalloprotease; Carboxypeptidase; Zinc; Dipeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:87874; Ace.
InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                         129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01401; Peptidase_M2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M61094; AAA37150.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M55333; AAA37149.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Transcription of testicular angiotensin-converting enzyme initiated within the 12th intron of the somatic ACE gene.", Mol. Cell. Biol. 10:4294-4302(1990).
                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                     20 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Howard T.E., Shai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90318396; PubMed=2164636;
                                                                                                                                                                                                                                                                                                                                                            Cocal
ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELULIAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS: 2 isoforms; testis-specific (shown here)
somatic (AC P09470), are produced by alternative splicing.
TISSUE SPECIFICITY: SPERWATOCYTES, ADULT TESTIS.
INDUCTION: EXPRESSION IS THOUGHT TO BE SUBJECT TO HORMONAL
                                                                                    AKTFDVSNFQNSSIKRIIKKLQNLDRAVLPPKELEEYNQILLDMETTYSLSNICYTNG--
                                                                                                                                         AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 139
                                                                                                                                                                                              TDEAKADREVEEYDRTAQVLLNEYAEANWQYNTNITIEGSKILLEKSTEVSNHTLKYGTR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF T VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.
CATALYTIC ACTIVITY: Release of a C-terminal dipeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligopeptide-|-xaa-xbb, when xaa is not Pro, and xbb is neither Asp nor Glu. Converts angiotensin I to angiotensin II. COPACTOR: BINDS 1 ZINC ION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A35655; A35655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGULATION BY ANDROGENS
                                                                                                                                                                                                                                                                                                                                  255;
                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.-Y., Langford K.G., Martin B.M.,
                                                                                                                                                                                                                                                                                                                                                      31.1%;
42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     84047 MW;
                                                                                                                                                                                                                                                                                                                            112;
                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                              Score 1334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZINC (CATALYT)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Testis; Signal; Alternative POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TESTIS-SPECIFIC ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANGIOTENSIN-CONVERTING ENZYME,
                                                                                                                                                                                                                                                                                                                                                                                                                                  16C817E7FBD09BD9
                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CATALYTIC) (BY SIMILARITY).

(KED (GLCNAC...) (POTENTIAL).

(KED (GLCNAC...) (POTENTIAL).

NKED (GLCNAC...) (POTENTIAL).

NKED (GLCNAC...) (POTENTIAL).

NKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CATALYTIC) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                      Ö.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC. .) (POTENTIAL)
(GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                6.7e-86;
                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                        Length 732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                             Gaps
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                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                             "The isolation of angiotensin-converting enzyme cDNA.";
J. Biol. Chem. 263:11021-11024(1988).
-i- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF
                                                                                                                                                                                                                                                                               Bernstein K., Martin B.M., Bernstein E.A., Linton J., Striker L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1989 (Rel. 10, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Anglotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
(ACE) (Dipeptidyl carboxypeptidase I) (Kininase II).
                                                                                                                                                                                                                                                                         Striker G
                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-332 FROM N.A., AND PARTIAL SEQUENCE MEDLINE-88298730; Pubmed-2841312;
                                                                                                                                                                                                                                                                                                                                                                                             Bernstein K.E., Martin B.M., Edwards A.S., Bernstein E.A.
                                                                                                                                                                                                                                                                                                                                                                        homologous
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89308599; PubMed=2545691;
                                                                                                                                                                                                                                                                                                                                                                                   "Mouse angiotensin-converting enzyme is
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P09470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACE_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           596 MKLGYSKPWPEAMKLITGQPNMSASAMMNYFKPLTEWLVTENRRHGETLGWPEYNWAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        558 LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       536 FDPGSKFHVPANVPYVRYFVSFTIQFQFHEALCRAAGHTGPLHKCDIYQSKEAGKLLADA 595
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                                                                                                                                                                                                                                                                                                                                                         Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLMKMALDKIAFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGD 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETY 497
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InterPro; IPR00130; 2n_Mrpeptdse.
Pfam; PF01401; Peptidase_M2; 2.
PRINTS; PR00791; PEPDIPTASEA.
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IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV
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                                     GDSWRSLYESDNLE------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL
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; PS00142; ZINC_PROTEASE; 2
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in; Transmembrane; Repeat; Signal; Alternative splicing.
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O1-0CT-1996 (Rel. 34, Last sequence update)
O1-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Angiotensin-converting enzyme (EC 3.4.15.1) (Dipeptidyl
Angiotensin-converting enzyme (EC 3.4.15.1) (Company of the converting enzyme (EC 3.4.15.1) (Company of the converting enzyme)
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Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                     1176 MKLGYSKPWPEAMKLITGQPNMSASAMMNYFKPLTEWLVTENRRHGETLGWPEYNWAP 1233
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                                                                                                                                                    entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme found in mammals.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Esther C.R.,
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InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 2.

Prodom; PD004184; PROSITE; PS00142;

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                                                AMKLGFSKPWPEAMQLITGQPNMSAEALMSYFEPLMTWLVKKNTENGEVLGWPEYSWTPY
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CYTOPLASMIC (POTENTIAL).
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MEROPS; M02.004; -.
InterPro; IPR001448; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 2.
PRINTS; PR00791; PEPDIPTASEA.
  TRANSMEM
                               DOMAIN
                                                                                                               SIGNAL
                                                                                                                                                                                       Prodom; PD004184; Peptidase_M2; 2. PROSITE; PS00142; ZINC_PROTEASE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-I - FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY THE TERMINAL HIS-LED, THIS RESULTS IN AN INCREASE OF T VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.

-I - CAPALYTIC ACTIVITY: Release of a C-terminal dipeptide, oligopeptide-[-xaa-xbb, when Xaa is not Pro, and Xbb i Asp nor Glu. Converts angiotensin I to angiotensin II.

-I - COFACTOR: BINDS 2 ZINC IONS (BY SIMILARITY)
                                                                                     CHAIN
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Angiotensin-converting enzyme, somatic isoform precursor (EC
                                                                                                                                                                     Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corvol P., Sternberg E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jafarian-Tehrani M., Listwak S.,
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Angiotensin converting enzyme and genetic hypertension: cloning rat cDNAs and characterization of the enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                      ycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a by non-profit institutions as long as i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specific; are produced by alternative splicing. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
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This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACE_RABIT STANDARD; PRT; 1310 AA.
P12822; 0072852;
01-OCT-1989 (Rel. 12, Created)
01-NOY-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Rabbit pulmonary angiotensin-converting enzyme: the NH2-terminal fragment with enzymatic activity and its formation from the native enzyme by M40H treatment.";

Arch. Biochem. Biophys. 227:188-201(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kumar R.S., Thekkumkara T.J., Sen G.C.;
"The mRNAs encoding the two angiotensian-converting isozymes transcribed from the same gene by a tissue-specific choice alternative transcription initiation sites.";
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Sen G.C.;
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"Use of alternative polyadenylation sites for tissue-specific transcription of two angiotensin-converting enzyme mRNAs.";
Nucleic Acids Res. 20:683-687(1992).
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MEDLINE=92178960;
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
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Eukaryota; Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Release of a C-terminal dipeptide, oliopeptide-1-xaa-xbb, when xaa is not pro, and xbb is Asp nor Glu. Converts angiotensin I to angiotensin II. COPACTOR: BINDS 2 ZINC IONS (BY SIMILARITY).

SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE BRODUCTS: 2 isoforms; somatic (shown here) a specific (AC P22968); are produced by alternative splici SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
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S35484; S35484.
                                                                                                                                                X62551; CAA44428.1;
M58579; AAA31151.1;
                                                                                                                                                                                                    requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 2.
PRINTS; PR00791; PEPDIPTASEA.

PD004184; Peptidase_M2;

MEROPS; M02.001; -MEROPS; M02.004; -

Hydrolase; PROSITE; PS00142;

ZINC_PROTEASE; 2.

Zinc; Dipeptidase;

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                                                                                                                                                                                                                                                           PTAWDL-GKGDFRILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAV
                                                                                                                                                                                                                                                                                                      PDKPNLDVTSTMVQKGWNATHMFRVAEEFFTSLGLLPMPPEFWAESMLEKPEDGREVVCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RA Kumar R.S., Thekkumkara T.J., Sen G.C.;

Ra Kumar R.S., Thekkumkara T.J., Sen G.C.;

Ra The mRNAs encoding the two angiotensin-converting isozymes are transcribed from the same gene by a tissue-specific choice of alternative transcription initiation sites.";

Ra J. Biol. Chem. 266:3854-3862(1991).

C. --- FUNCTION: CONVERTS ANGIOTENSIN I TO ANGIOTENSIN II BY RELEASE OF THE TERMINAL HIS-LEU, THIS RESULTS IN AN INCREASE OF THE VASOCONSTRICTOR ACTIVITY OF ANGIOTENSIN.

C. --- CATALYTIC ACTIVITY: Release of a C-terminal dipeptide, Coliopeptide-|-xaa-xbb, when xaa is not Pro, and xbb is neither C. --- CATALYTIC ACTIVITY angiotensin I to angiotensin II.

C. --- CATALYTIC ACTIVITY SAME ANGIOTENSIN I to angiotensin II.

C. --- SUBCELULIAR LOCATION: Type I membrane protein.

C. --- SUBCELULIAR LOCATION: Type I membrane protein.

C. --- SUBCELULIAR LOCATION: Type I membrane protein.

Somatic (AC P12822); are produced by alternative splicing.

--- TISSUE SPECIFICITY: SPERMATOCUTES. ADDUCT TESTIS.
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P22968;
P22968;
P22968;
P23968;
P2406-1991 (Rel. 19, Created)
P2507 (Rel. 19, Last sequence update)
P2507 (Rel. 41, Last annotation update)
P2507 (Rel. 19, Last sequence update)
P2508 (Rel. 19, Last seque
                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                            entities requires a license agreement (some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-117 FROM N.A. MEDLINE=91139683; PubMed=1847388;
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Mammalia; Eutheria; Lagomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDUCTION: EXPRESSION IS THOUGHT TO BE SUBJECT REGULATION BY ANDROGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration -
sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YE--WND-----NEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVRVANLKPRISFNFF
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EMBL; J05041; AAA31153.1; EMBL; M58580; AAA31152.1; PIR; A34402; A34402.

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Pfam; PF01401; Peptidase_M2; 1.
PRINTS; PR00791; PEPDIPTASEA.
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PROSITE; PS00142; ZINC_PROTEASE; 1.
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                                                                                                                                                                                                                                       DFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPD
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WPOYTWTPNSARS 664
                                                                           TEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQN--KNSFVG
                                                                                                      CPPAPRSQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCKAAGHTGPLHTCDIYQS
                                                                                                                                                                                     FQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGV
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                                                                                                                                                                                                                                                                    EEADKFFISLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNME
                      W-STDWSPYADQS 617
                                                 KEAGKRLADAMKLGYSKPWPEAMKVITGQPNMSASAMMNYFKPLMDWLLTENGRHGEKLG
                                                                                                                              VEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNS
                                                                                                                                                           -GGGYEHDINFLMKMALDKIAFIPFSYLVDEWRWRVFDGSITKENYNQEWWSLRLKYQGL
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Pred. No. 2
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BY SIMILARITY.
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NC (CATALYTIC) (BY SIMILARITY).

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ZINC (CATALYTIC) (BY SIMILARITY)
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N-LINKED (GLCNAC. . .) (POTENTIAL

(POTENTIAL)

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ZINC (CATALYTIC) (BY SI
BY SIMILARITY.

SIMILARITY).

ENZYME

SIGNAL

Glycoprotein; Hydrolase;

Signal

POTENTIAL

Metalloprotease;

Carboxypeptidase; Zinc; Dipeptidase;

CARBOHYD

CARBOHYD

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Q10714; Q27572;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carboxypeptidase ANCE OR RACE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \label{eq:medline} $$\operatorname{MEDLINE}=96028519;$$ $\operatorname{PubMed}=7547464;$$ $$\operatorname{Tatei}$$ K., $\operatorname{Cai}$$ H., $\operatorname{Ip}$ y.T., $\operatorname{Levine}$ M.; $$ $^{\mathtt{Race}}: a Drosophila homologue of the angiotensin converting enzyme."; $$ $\operatorname{Mech}. Dev. 51:157-168(1995). $$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cornell M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U25344; AAB02171.1; -. EMBL; U34599; AAC46902.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            proDom; pD004184; Peptidase_M2; 1.
proSITE; pS00142; ZINC_PROTEASE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; M02.003;
                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00791; PEPDIPTASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0012037; Ance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: Release of a C-terminal dipeptide, chigopeptide-|-xaa-xbb, when xaa is not Pro, and xbb is neither Asp nor Glu. Converts angiotensin I to angiotensin II. COFACTOR: BINDS 1 ZINC ION.

SUBCELLULAR LOCATION: Extracellular.

DEVELOPMENTAL STAGE: EXPRESSED IN THE AMNIOSEROSA DURING GERM BAND ELONGATION, SHORTENING AND HEART MORPHOGENESIS. EXPRESSED IN MIDGUT THROUGHOUT EMBRYOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: MAY PLAY A ROLE IN THE CONTRACTIONS OF THE HEART,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
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AC 01071:
AC 01071:
AC 01070:
DT 01-NO:
DT 01-NO:
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DE Carbo:
GN ACE:
OS Haema
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                                                                                                                                           ACE_HAEIE
Q10715;
01-NOV-1997
         Eukaryota; Metazoa; Arthropoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
Musconorpha; Muscoidea; Muscidae; Haematobia
                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
   NCBI_TaxID=34678;
                                                                                  carboxypeptidase I) (Kininase
                                                                                                Angiotensin-converting enzyme
                                                       Haematobia irritans
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                                                                                                                                                                                                                                                                              N--KNSFVGWST 608
                                                                                                                                                                                                                                                                                                  LDNCDIYGSARAGAAFHNMLSMGASKPWPDALEAFNGERIMSGKAIAEYFEPLRVWLEAE
                                                                                                                                                                                                                                                                                                                             LHKCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQ 598
                                                                                                                                                                                                                                                                                                                                                                                     VGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALC-QAAKH-----EGP
                                                                                                                                                                                                                                                                                                                                                                                                                   K-DYVRDDEARINQLFLTALDKIVFLPFAFTMDKYRWSLFRGEVDKANWNCAFWKLRDEY
                                                                                                                                                                                                                                                                                                                                                         SGIEPPVVRSEKDFDAPAKYHISADVEYLRYLVSFIIQFQFYKSACIKAGQYDPDNVELP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TQDQLFTVHHELGHIQYFLQYQHQPFVYRTGANPGFHEAVGDVLSLSVSTPKHLEKIGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KMFQMGDDFFTSMNLTKLPQDFWDKSIIEKPTDGRDLVCHASAWDFYLIDDVRIKQCTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGK-GDFRILMCTKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQ 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKVKVCDYKDSTKCDLALDPETEEVISKSRDHEELAYYWREFYDKAGTAVRSQFERYVEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELAKFMKEVASDTTKFQWRSYQSEDLKRQFKALTKLGYAALPEDDYAELLDTLSAMESNF 127
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71025 MW;
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                                                     exigua (Buffalo fly)
                     Arthropoda; Mandibulata; Pancrust
Neoptera; Endopterygota; Diptera;
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WAYG -> GPMR (IN REF. 3).
C -> S (IN REF. 3).
A -> G (IN REF. 3).
S -> T (IN REF. 3).
V -> M (IN REF. 3).
R -> A (IN REF. 3).
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Pred. No. 6.9e-69;
                                                                                 precursor II).
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                                    Pancrustacea;
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                     Brachycera;
                                   Hexapoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001548; Peptidase_M2; InterPro; IPR000130; Zn_MTpeptdse. Pfam; PF01401; Peptidase_M2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L43965; AAA70427.1; -
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SEQUENCE FROM N.A.
MEDLINE-96215437; PubMed-8647080;
                                                                                                                                                                                                                                                                                                                                                        128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wijffels G.L., Fitzgerald C., Gough J., Riding G.A., Elvin C., Kemp D.J., Willadsen P.;
                                                                                                                                                                                                                                                                                                                                                                                                            83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 LLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGD
                                                                       YRLNKFYGDEVVSKTGPLPMHLLGNMWAQQWSSIADIVSPFPEKPLVDVSDEMVAQGYTP
                                                                                                                         AKLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDA
                                                                                                                                                                             NTKSAKLNNFTDGAEVWLDEYE------DATFEDQLEAIFEDIKPLYDQVHGYVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POSTERIOR REGION OF THE MIDGUT. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: EXPRESSED IN THE COMPOUND GANGLION
                                                                                                                                                                                                                               KNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIED-VEHTFEEIKPLYEHLHAYVR
                                                                                                                                                                                                                                                                                      AKVRVCDYKNSAKCDLSLDPEIEEIITKSRDPEELKYYWTQFYDKAGTPTRSNFEKYVEL
                                                                                                                                                                                                                                                                                                                                       STGKVCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligopeptide-|-Xaa-Xbb, when Xaa is not Pro, and Xbb i Asp nor Glu. Converts angiotensin I to angiotensin II. COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                             KWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILAGLAVCHGATKEEIVATEYLQNINKELAKHTNVETEVSWAYASNITDENERLRNEISA
                                                                                                                                                                                                                                                                                                                                                                                            ENAKFLKEVAKDIQKFNWRTYGSADVRRQFKSLSKTGYSALPAEDYAELLEVLSAMESNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      611 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal. 17
1 18 611
367 367
368 368
371 371
53 53
196 196
531 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70505 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZINC (CATALYTIC) (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANGIOTENSIN-CONVERTING ENZYME.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A43D6DF5A83ECB53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.2e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                        363
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                                                                                                                                                                                                                                                                                      187
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γ Вþ Ş B

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             RX MEDLINE=98044045; Pudmado=93845/;
RA Kunst F., Ogasawara N., Moscer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Brans M., Brignell S.C., Bron S.,
RA Boroillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Broillet S., Bruschi C.V., Caldwell B., Child S.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Ghim S.Y., Glaser P., Goffeau A., Goliphthy E.J., Garandi G.,
RA Gliseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,
RA Joris B., Karamata D., Kasahara Y., Klaerr Blanchard M., Klein C.,
RA Hilbert H., Holsappel S., Hosono S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Paresecan E., Pujic P., Purnelle B., Ropport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Ra Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Taxahashi H., Takemaru K.,
RA Takeuchi M., Tamboshi A., Tanaka T., Taxahashi H., Takemaru K.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vasaumoto K., Yata K.,
RA Tosato V., Ghiyama S., Vandenbol M., Vannier F., Vasarotti A.,
RA Tosato V., Ghiyama S., Vandenoto H., Wanier F., Vasarotti A.,
RA Tosato V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P50848;
01-OCT-1996
01-OCT-1996
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical metalloprotease ypwA (EC 3.4.24.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPWA_BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      536 PLDNCDIYGSKEAGKLFENMLSLGASKPWPDALEAFNGERIMIGKAIAEYFEPLRVWLE 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 LKMFQMGDDFFQSMGLKKLPQEFWDKSILEKPDDGRDLVCHASAWDFYLTDDVRIKQCTR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the serA and kdg loci cloned in a Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorokin A.V., Azevedo V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96349105; PubMed=8760912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=168 / Marburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence analysis of the Bacillus subtilis chromosome region between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
"The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLHKCDISNSTEAGOKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLK 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSGIEPPVVRTEKDFDAPAKYHVSADVEYLRYLVSFIIQFQFYKSACITAGEYVPNQTEY 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAA-----KHEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKRE 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LK-NYVSDNEARINGLFLTALDKIVFLPFAFTMDKYRWALFRGQADKSEWNCAFWKLREE 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTQDQFFTVHHEMGHIQYFLQYQHQPFVYRTGANPGFHEAVGDVLSLSVSTFKHLERVGL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cloned in a yeast artificial chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zumstein E., Galleron N., Ehrlich S.D.,
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 390:249-256(1997).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L77246; AAA96610.1;
EMBL; Z99115; CAB14125.1;
MEROPS; M32.UPW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00998; CRBOXYPTASET.
PROSITE; PS00142; ZINC_PROTEASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L47838; AAB38482.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Hydrolase; Metalloprotease; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SubtiList; BG11458; ypwA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02074; Peptidase_M32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 YEEYVVL--KNEMA--RANHYEDYG-------DYWRGDYEVNGVDGYDYS 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 YKEYYILCSKAETAWEEAKGKSDFSLFSPYLEQLIEFNKREITYW------GYQ-- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 RGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNL 278
                                                                                                                                                                                                                                                                                                                                                            332 MLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTA----HHEMGHIQYD--MAY 385
                                                                                                                                                                                                                                                                                                                                                                                                                             279 YSLTVPF-----GQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLPNMTQGFWENS 331
                                                451 HPIK-----OWLTEKVHIHGKRKKPLDIIKDATG-EELNVRYLIDY 490
                                                                                   540 HKCDISNSTEAGOKLENMLRL-GKSEPWTLALENVVGAKNMNVRPLLNY 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                              KEATIPLVKQVTASGNKP-----DTSFITKAFPKEKQKELSLYFLQELGYDF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----EHPYDALLDLFE---PGVTVKVLD----
                                                                                                                     I---TPQTDAEGILQDVHWAGGDFGYFPSYALGYMYAAQLKQKMLEDLPEFDALLERGEF 450
                                                                                                                                                     VVEPVPHDETYCDPASLFHVSNDYS-FIRYYTRTLYQFQFQEALCQ-----AAKHEGPL 539
                                                                                                                                                                                         QEDNETEINFLLKQA--LTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVG 486
                                                                                                                                                                                                                                                       ALSGTNLSDGASMGTHESQSLFYENFTGRNKHFWTPYYKKTQEASPVQFKDISL--DDFV 336
                                                                                                                                                                                                                                                                                         AAQPFLLRNGANEGFHEA-----VGE-----IMSLSAATPKHLKSIGLLSPDF- 428
                                                                                                                                                                                                                                                                                                                           ---DGGRLDETV-HPFATTLNRGDVRV--TTRYDEKDFRTAIFGTIHECGHAIYEQNIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPRO001333; Peptidase_M32.
IPRO00130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.1%; 20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58174 MW; A7489BABEFA38F82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65; Mismatches 164; Indels 142; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 135; DD -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZINC (CATALYTIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZINC (CATALYTIC) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FALSE_NEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---QLFAEL 177
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GLGB_BACSU

P39118; GLGB_BACSU

STANDARD;

627

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01-FEB-1995 01-FEB-1995 15-JUN-2002

(Rel. 31, Created)
(Rel. 31, Last sequence update) (Rel. 41, Last annotation update)

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RA Kunst F. Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursler L., Brans A., Braun M., Brignell S.C., Bros. S.
RA Brouillet S. Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Gilm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Gilm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Gilm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Taya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle B., Rapport G., Rey M., Reynolds S.,
RA Parro V., Fohl T.M., Portetelle B., Rapport G., Rey M., Reynolds S.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serore R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serore M., Sadaie Y.,
RA Serokin A., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Yoshida K., Vohlama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
The complete genome sequence of the Gram-positive bacterium Bacillus
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                 Nature 390:249-256(1997).

-!- FUNCTION: CATALYSES THE FORMATION OF THE ALPHA-1,6-GLUCOSIDIC LINKAGES IN GLYCOGEN BY SCISSION OF A 1,4-ALPHA-LINKED OLIGOSACCHARIDE FROM GROWING ALPHA-1,4-GLUCAN CHAINS AND THE SUBSEQUENT TRANSFER OF THE OLIGOSACCHARIDE TO OTHER PARTS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequencing and functional annotation of the Bacillus subtilis genes in the 200 kb rrnB-dnaB region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98048467; PubMed=9387221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microbiology 143:3431-3441(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Microbiol. 11:203-218(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Glycogen in Bacillus subtilis: molecular characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94195107; PubMed=8145641;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis
Bacteria; Firmicui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1423;
                                                                                                                                                                               CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
                                                                              SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                 INDUCTION: EXPRESSED EXCLUSIVELY ON MEDIA CONTAINING CARBON SOURCES THAT ALLOW EFFICIENT SPORULATION.
                                                                     KNOWN AS THE ALPHA-AMYLASE FAMILY
                                                                                                                                              PATHWAY: Glycogen biosynthesis; third step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding enzymes involved in glycogen biosynthesis and
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    531 F-SFIRYGQKH---
                         643 FRSSVAYAMRQYFLKVKNQMTLFGEEDVRVANLKPRISFNFFVTAP 688
                                                     474 DTEQ---LDWFLDSFPMHQKASVFTQDLLRFYQKSKILYEHDHRAQSFEWIDVHNDEQSI
                                                                                                                                 426
                                                                                                                                                     552 QKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNY----
                                                                                                                                                                                       391 PEERRHC-----HQLISFSLL--
                                                                                                                                                                                                            492 PHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAG
                                                                                                                                                                                                                                         334 KKLNQTMREAYPHYMMIAEDSTEWPQVTGAVEEGGLGFHYKWNMGW---MNDVLKYMETP 390
                                                                                                                                                                                                                                                                       440 LKQALTIVGTLPFTYML--EKWRWMVFKGEIPKD-----QWMKKWWENKREIVGVVEPV 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 WTNLYSLTVPEGQKPNIDVTDAMVDQA------WDAQRIFKEAEKFFVSVGLPNNT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 LSQTLIPYIKKHGFTHIELLPVYE--HPYDRS------WGYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SubtiList; BG10907; glqB.
InterPro; IPR000461; Alpha_amylase
InterPro; IPR004193; Isoamylase_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 GYSWQDQKWQKKQKAKTLYEKPVFI-----YELHLGSWK-----KHSDGRHYSYKE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 LWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQ 221
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PIR; S36624; S36624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 DFNSWSGEEHVMHRVNDNGIWTLFIPGIGEKER-----YKYEIVTN------N 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 NYNTNITEENVQNMNNAGDKWSAFL-----KEQSTLAQMYPLQEIQNLTVKLQLQALQQN 103
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                                                                                                                   KK--SLLNKMPGDYW-------QKFAQYRLLLGYMTVHPGKKLIFMGSEFAQFDEW-K 473
                                                                                    DQNKNSFYGWSTDWSPYADQSI-----KYRISLKSALGDKAYEWND---NEMYL 642
                                                                                                                                                                                                                                                                                                                                 YDMAYAAQPFLLRNGANEGFH-EAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFL 439
                                                                                                                                                                                                                                                                                                                                                                --LYEYKEERDREN------WLWGTANFDL---GKPEVHSFLISNALYWAEFYHI-
                                                                                                                                                                                                                                                                                                                                                                                             QGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAH----HEMGHIQ 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIEDV----EHTFE--EIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GETRLKADP-----YAIYS-----125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMAN--SLDYNER 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00128; alpha-amylase; PF02922; isoamylase_N;
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627 AA;
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73665 MW;
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-----GEALVIICNFTPVVYHQYDVGVP 563
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RESULT 13
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P30195;
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MEDLINE=92155237; PubMed=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermidis.
Plasmid pTu 32.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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01-APR-1993 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Analysis of genes involved in the biosynthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goetz F., Entian K.-D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schnell N., Engelke G., Augustin J., Rosenstein R., Ungermann V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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SUBCELLULAR LOCATION: POSSIBLY ASSOCIATED WITH, AND ANCHORED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: TO B. SUBTILIS SPAB AND L. LACTIS NISB.
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                                                                                                                                                                                                                                                              DKSKRLNTILNTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRS
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                                                                                                                                                                                                                                                                                                                                                                                             ISEAAYILWLLSPNHFGTKTIRNYHEFFMDKYGFEQLVNLKQLLSDINGFGYPKKDSYSF 379
                                                                                                                                                                                                                                                                                                                                                                                                                            MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHE-----AEDL--FYQSSLASWNY 50
TEEGIDSLPFCPRIIYKNIILKPATWKINSEMFSE---TENWLNRFATI-REKWHIPKDV
                                                                                                                                                                                                                             EVGKQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTF
                                                                                                                                                               EEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPN
                                                                                                                                                                                                --GNSIKG-YEDFAVISPILGSFNAGATFGRF-TGNFNIK--
                                                               IDINDIFIGATENKLYLYSEKHDSRIVFVSNSMENYEFGSELYKFLREISFEKTKFIQPI
                                                                                                IDVTDAMVDQAWDAQRIFKE---AEKFFVSVGLPNMTQG------
                                                                                                                                -----HYNNYMNENGLEISQLNEGPLNSRNVNILNN--NRIYNTCLNLNLP----KSD
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                                  -----VQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGHIQYDM
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25, Last sequence update)
40, Last annotation updat
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RESULT 14
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Beta-galactosidase (EC 3.2.1.23) (Lactase).
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                                                                                                                     EMBL; AJ000733; CAA04267.1; -.
                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                           use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                 Strey J
                                                                                                                                                                                                                                                                                                                              STRAIN-DSM 319;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1404;
                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                               Bacillus megaterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                692 SDIIP-----RTEVEKAIRMSRSRINDAF---RLNDNSLEFLGIQ
                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --LSAATPK-----HLK---SIGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLE 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPYADQSIKVRISLKSALGDK 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYCLLNSELYDYSIVDYVPEVYRYGGPHVIEDIENFFMYDSLL--SINIIQSE-FKIPKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLGKSEPWTLALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 962
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                                                                                                                                                                                                                                                                                                                                                                                    Bacillales; Bacillaceae;
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InterPro; IPR004200; Bgal_small_C.
InterPro; IPR004199; Bgal_small_N.
InterPro; IPR0061649; GH_2.
InterPro; IPR001649; GH_2.
Pfam; PF00703; Glyco_hydro_2_C; 1.
Pfam; PF02836; Glyco_hydro_2_C; 1.
Pfam; PF02837; Glyco_hydro_2_N; 1.
Pfam; PF02939; Bgal_small_N; 1.
Pfam; PF02930; Bgal_small_C; 1.

P00722;

1BGL.

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RRA RRA
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OSH2_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                         OSH2_YEAST STANDARD; PRT; 1283 AA. Q12451; P89891; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                       Oxysterol-binding protein homolog OSH2 OR YDL019C OR D2845.
SUBCELLULAR LOCATION
                          Submitted (JUL-1996) to
                                          Urrestarazu L.A.,
                                                            STRAIN=S288c;
                                                                         SEQUENCE FROM N.A.
                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Glycosidase.
ACT_SITE 481 481
ACT_SITE 547 547
SEQUENCE 1034 AA; 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00132; GLHYDRLASE2.
PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1;
PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2;
                                                                                                                                                                                                                                                                                                                                                                                 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 LNYFEHDTQDLTFEVMLYDANAQEVLQAPLQTNLSVSDQRTVSLRTHIKSPAKWSA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 LDKFNHEAEDLFYQSSL------ASWNYNTNITEENVQNMN---NAGDKWSAFLKE 75
                                                                                                                                                                                                                                                                                                                                                                                                      TVE----KNG-----ELVEKHASLLNVAPDGTDELTLSYPLYEQENETD-EFVLTLSLR
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLLKQALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NID----VTDAMVDQAWDAQRIFKEAE---KFFVSVG-----LPNMTQGFWENSMLTDPGNV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSTLAQMYPLQEIQNL-TVKLQLQALQQNGSSVLSEDKSK---RLNTILNTMSTIYSTGK 131
                                                                                                                                                                                                                                                                                                                                                                               I 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPKIAEVKKCYQPVKWTAVDPAKGKFAV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKAV-----CH-PTAW----DLGKGDFRILMCTKVTMDDFLTAHHEMGHI-----QYDMAY 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILQGGFIWD-----WKDQALQATAEDGTSYLAYGGDFGDTPN-DGNFCGNGLIFADGTA 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKP 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NESFGGENFQHMYTFFKEKDSTRLVHYE--GIFHHRDYDASDIESTMYVKP---ADVE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1034 AA; 118673 MW; 38644C9A649415E9 CRC64;
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                                          Andre
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19.2%;
                          B., Vissers S.; the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTON DONOR (BY SIMILARITY). NUCLEOPHILE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50088; ANK_REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION;
PROSITE; PS01013; OSBP; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipid transport; Transport; ANK repeat; Repeat; Golgi stack.
REPEAT 106 134 ANK 1.
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EMBL; Z74067; CAA98578.1;
EMBL; Z48432; CAA88340.1;
SGD; S0002177; OSH2.
       247
                                644 KRLVDMVSKQGDVNNVW-----VQSVKELEMELSNKTERLASIDKERRGLKKILH----K
                                                                         193
                                                                                                           584
                                                                                                                                             156
                                                                                                                                                                             528
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                                                                                                                                                                                                                                                                                                            412 ALISHSKTQGSLPEASQYYQHTLHKE----VIQPSSVSLYRRPSNNLSVVSSEIQLNDNLT 468
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InterPro; IPR001849; PH.
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Beh C.T., Cool L., Phillips J., Ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Levine T.P., Munro S.;
"Dual targeting of Oshlp, a yeast homologue of oxysterol-binding protein, to both the Golgi and the nucleus-vacuole junction."; Mol. Biol. Cell 12:1633-1644(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002110; ANK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beh C.T., Cool L., Phillips J., Rine J.; Overlapping functions of the yeast oxysterol-binding protein
                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                            10 SLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASW---NYNTNITEENVQ---NMN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic. When bound translocate to the periphery of Golgi membrane SIMILARITY: BELONGS TO THE OSBP FAMILY. SIMILARITY: CONTAINS 2 ANK REPEATS. SIMILARITY: CONTAINS 1 PH DOMAIN.
     KLMNAYPSYISPIGC-----
                                                                                                                                      LDYNERLWAWESWRS-----EVGKQLRPLYEEYVVLKNEMAR-----
                                                                                                                                                                      NGANLSQSNTTTGSTASLSDNNYIDNFEGDEANSDDEEEDL----GINFDRDEEYIKAQY 583
                                                                                                                                                                                                                                                                          NAGDKWSAFLKEQSTLAQMYP-----LQEIQNLTVKLQLQALQQNGSSVLSE-DKSK 114
                                                                -----ANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRA
                                                                                                    GPYKEKLDMYEQAISIELSSLIELIEQEEPSPEVWLTIKKSLINTSTIFGKLKDLTYKRD 643
                                                                                                                                                                                                         RLNTILNTMSTIYST------
                                                                                                                                                                                                                                          ESGKRFVSKMIENRLDGSKTPVGVHTGSALQRVRSSNT-LKSNRSMQSGSGVASPIDKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF01237; Oxysterol_BP; SM00248; ANK; 2. SM00233; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00169; PH; 1
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                   Conservative 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235
386
                                                                                                                                                                                                                                                                                                                                                                                                   2.8%; Score 119.5;
18.9%; Pred. No. 2.5
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-LPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAM
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                                                                                                                                                                                                        -GKVCNPDNPQECLLLEPGLN-----EIMANS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                    D521957460E7F7C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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         Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brown D., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., McLean J., Wooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q10064;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein CIF5.11c in chromosome I
SPACIF5.11C.
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                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 schizosaccharomyces.
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                                                                                                                                                                                                                                                  MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4896;
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Hypothetical protein; Transferase; Kinase.

DOMAIN 3324 3655 PI3K/PI4K (BY SIMILARITY)
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Pfam; PF02260; FATC; 1.
SMART; SM00146; PI3KC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z68136; CAA92239.1; -.
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-!- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2776
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                                                                          2906 EANQAFATAVQIDIGSG-
                                                                                                                                                                                                                            2847 QEAFLKLREQAECHYESPSEMOLGLEVINNTNLMYFRNRQKAEFFTLKGMFQN-RLGEKD 2905
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   398 --EGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYM 455
                                                                                                                                                                                                                                                                                               294 TDAMVDQAWDAQRIFKEAEKFFVSVGLPNMT------QGFWENSMLTDPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSINKVFLPLVSIAQQSTNKSNTNSVSYLYRGYHEL-----
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                                                                                                                                             NVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGAN 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEI 233
                                                                                                                                                                                                                                                                                                                                                                                  -----AWIINRE-AHVARVHHLPEVCINQL----TKIYTL-----PNIEI 2846
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IPR000403; PI3_PI4_kinase
IPR001440; TPR.
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SALE ELECTION OF THE PROPERTY 
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DYHC_PARTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kandl K.A., Forney J.D., Asai D.J.;
"The dynein genes of Paramecium tetraurelia: the structure and expression of the ciliary beta and cytoplasmic heavy chains.";
Mol. Blol. Cell 6:1549-1562(1995).
-I- FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS A MOTOR FOR THE INTRACELLULIAR RETROGRADE MOTILITY OF VESICLES AND
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
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Probable methylenetetrahydrofolate reductase (EC 1.5.1.20). C06A8.1.

15-JUL-1999 (Rel. 38, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)

RESULT 18 MTHR_CAEEL

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MTHR_CAEEL

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                                                                          NNIQSKI----QQDERYLNQQIQEIEEQWKTSKPDSGDCSPNEAEQILKSLNEQLISVQE 1236
                                                                                                                       LKVKNQMILFGEEDVRVANLKPRISFNFFVTAPKNVSDIIPR--TEVEKAIRMSRSRIND 713
                                                                                                                                                              K-KFPGWSADIESFKNGQKVLDRQRYQYPGDWLSFEQVEMQWNQFKQIRSKKLQSQESEM 1180
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Pfam; PF02219; MTHFR; 1.
TIGRFAMS; TIGRO0677; fadh2_euk; 1.
Oxidoreductase; Flavoprotein; FAD;
Oxidoreductase; Flavoprotein; FAD;
663 AA; 75486 MW; EA9
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InterPro; IPR003171; Mehydrof_redctse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WormPep; C06A8.1; CE30593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 QRIFKEAEKFF-----VSVGLPN------MTQG-----FWENSMLTDPGNVQK- 341
                                                                                                                                                                                                                                                     461
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                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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                                  632 AYEWNDNEMYLFRSSVAYA-MRQYFLK----VKN---QMILFGE-----EDVRVANLKPR 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
CATALYTIC ACTIVITY: 5-methyltetrahydrofolate + NADP(+) = 5,10-
methylenetetrahydrofolate + NADPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: Folate metabolism.
SIMILARITY: BELONGS TO THE METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.5.1.20/EC 1.7.99.5) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: FAD (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                    TSSSSIAASMLDYCGVDTMLHMTCVQYNKADTLKHLEQAKAMGLRSILALRGDLPPGTEL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERLIDEKQQFFSLEEFPPRFVNGVPNFLERVERLSEGGSVFVDMTWH--MGSDPANVDKV 120
                                                                                                                                                                                                                    AKLSQLEIP-
                                                                                                                                                                                                                                                     WMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTL 520
                                                                                                                                                                                                                                                                                       TQLFFEAETFEKFVRDCREIGITQP------IPGIMPIMGYESIKRI
                                                                                                                                                                                                                                                                                                                           GEIMSLSAATPKHL---KSIGLLSPDFQEDNETEINFLLKQALTIVGTLPFT-YMLEKWR
                                                                                                                                                                                                                                                                                                                                                             EDTHQFRALDMIRWIREEYGNYFSIGCAGYPLGHPQAP-SYKADLMYLKAKCDAGANFVI 239
                                                                                                                                                                                                                                                                                                                                                                                                ----FRILMCTKVTMDDFLT-----AHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAV
                                                                    FPWKNRSQHPIRCLESVRPIY-W--SFRPRSYITRTRDWDQFPNG---
                                                                                                      VGAKNMNVRPL--LNYFEPLFTWLKDQNKNSFVGWSTDWSPYADQSIKVRISLKSALGDK 631
                                                                                                                                        IE----MCRRL-----LDNGTAPSIHLYTMNREGSIREILKSLGLWKLEGDRV
--RWGNS----SSPAFGDVSSYYLSNLTTVRNADDRLAMFGANIESFEDVK-----R
                                                                                                                                                                              YQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLGKSEP-----WTLALENV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---AVCHPTAWDLGKGD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.7%; Score 118;
18.3%; Pred. No. 1
                                                                                                                                                                                                                    --QHILDDLEPIKHD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 663;
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                                                                                                                                                                                                                    ----DDAVQKYGTERC
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AKA9_HU
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AKAP9 OR AKAP450 OR AKAP350 OR KIAA0803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin J.W., Wyszynski M., Madhavan R., Sealock R., Kim J.U., Sheng I "Yotiao, a novel protein of neuromuscular junction and brain that interacts with specific splice variants of NMDA receptor subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT GLN-1347 INS MEDLINE=99219864; PubMed=10202149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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nings K., Sutterer C., Becker M., Hawkins M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
[7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and characterization of a cDNA encoding an A-kinase anchoring protein located in the centrosome, AKAP450."; EMBO J. 18:1858-1868(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Witczak O., Skaalhegg B.S., Keryer G., Bornens M., Jahnsen T., Oerstavik S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                   associated with centrosomes.";
J. Biol. Chem. 274:3055-3066(1999)
                                                                                                                                                                                                                                                                                        Schmidt P.H., Dransfield D.T., Claudio J.O., Hawley R.G. Trotter K.W., Milgram S.L., Goldenring J.R.;
                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99115654; PubMed=9915845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anchors multiple signaling enzymes to centrosome and the golgi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kemmner W.A., Deiss S., Schwarz U.;
"Cloning of Hyperion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apparatus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takahashi M., Shibata H., Shimakawa M., Miyamoto M., Mukai H., ("Characterization of a novel giant scaffolding protein, CG-NAP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Brain
                                                                                                                                SEQUENCE OF 1802-3876 FROM N.A. (ISOFORM 5)
                                                                                                                                                                                                                                                             "AKAP350, a multiply spliced protein kinase A-anchoring protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99287934; PubMed=10358086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AUG-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274:17267-17274(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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RESIDENCE OF 17-1800 FROM N.A.

AN U.X., Graves T., Bradshaw H.;

RA WU.X., Graves T., Bradshaw H.;

RA WU.X., Graves T., Bradshaw H.;

RU.X., Graves T., Rushing T., Rushing Gold Arbaratus Where Physiological SC PHOSPHATASES ON CENTROSOME AND GOLGI APPARATUS WHERE PHYSIOLOGICAL CONTROLOGICAL SUBSTRATES. ISOFORM 4/YOTIAO IS ASSOCIATED WITH THE N-METHYL-D-SUBSTRATES. ISOFORM 4/YOTIAO IS ASSOCIATED WITH THE N-METHYL-D-SUBSTRATES RECEPTOR AND IS SPECIFICALLY FOUND IN THE NEUROMUSCULAR COLOR MAY BE TO ORGANIZE POSTSYNAPISE SEXPLAINING THAT ITS COLOR MAY BE TO ORGANIZE POSTSYNAPISE SPECIALIZATIONS.

CI. SUBBUNIT: INTERACTS WITH THE RECULATORY REGION OF PROTEIN KINASE NOTHING THE IMMATURE MON-PHOSPHORYLATED FORM OF PRC EPSILON.

CI. SUBBURIT: INTERACTS WITH THE RECULATORY REGION OF PRC EPSILON.

CI. SUBBURIT: INTERACTS WITH THE RECULATORY REGION OF PRC EPSILON.

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CI. SUBBURIT: INTERACTS WITH THE RECULATORY REGION OF PRC EPSILON.
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                                                                                                                                                                                          EMBL; AJ131693; CAB40713.1; ...
EMBL; AJ019691; BAA78718.1; ...
EMBL; AJ010770; CAB409361.1; ...
EMBL; AF026245; AAB86384.1; ...
EMBL; AF083037; AAD22767.1; ...
EMBL; AC004013; AAB96867.1; ALT_FRAME.
                                                                DOMAIN
                                                                                DOMAIN
                                                                                                           Coiled
                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                              DOMAIN
                                                                                                                                           Genew;
                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Prediction of the coding sequences of unidentified human genes, XI. The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99087487; PubMed=9872452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 2212-3911 FROM N.A. (ISOFORM 2/3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Milgram S.L., Goldenring J.R., Schmidt P.H.; "AKAP350: A multiply spliced family of proteins with centrosomal association.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagase T., Ishikawa K.-I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 2157-3911 FROM N.A. (ISOFORM 6)
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                                                                                                                                                                                                                                                                                                                                                                                                                               CAUTION: REF.6 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO TWO FRAMESHIFTS IN POSITIONS 3782 AND 3811.
CAUTION: REF.9 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FOUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXPRESSED IN SKELETAL MUSCLE AND IN PANCREAS.

DOMAIN: RII BINDING SITE, PREDICTED TO FORM AN AMPHIPATHIC HELIX, COULD PARTICIPATE IN PROTEIN-PROTEIN INTERACTIONS WITH A COMPLEMENTARY SURFACE ON THE R-SUBUNIT DIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC IN PARIETAL CELLS.
ALTERNATIVE PRODUCTS: 6 ISOFORMS; 1 (SHOWN HERE), 2, 3/CG-NAP, 4/YOTIAO, 5 AND 6/AKAP350; ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                     FRAMESHIFTS IN POSITIONS 29, 1653, 1699 AND 1735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: WIDELY EXPRESSED.
                                                                                                                                                                                     AC004013;
AF091711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           large proteins in vitro
                                                                                                                                                         AC000066;
                                                                                                                                                                       AB018346;
                                                                                                             coil;
                                                                                                                                         HGNC:379; AKAP9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5:277-286(1998).
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    2554
164
944
1100
1253
1336
1434
                                                                                                         Alternative
                                                                                                                                                      AAC60380.1;
                                                                                                                                                                       BAA34523
                                                                                                                                                                                    AAD39719.1;
                                               914
1022
1185
                                                                                                        splicing;
              PALICLED; POLYMOZPHISM.

PKA-RII SUBUNIT BINDING DOMAIN.

COILED COIL (POTEMPIAL).

COILED COIL (POTEMPIAL).
                                                                                                                                                  ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suyama M., Kikuno R., Miyajima
COIL
            (POTENTIAL)
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                                                                                      1154 ALCSLKEELIFAQEEKIKELQKIHQLELQTMKTQETGDEGKPLHLLIGKLQKAVSBECSY 1213
                                                                                                                                                 1095 SLRATQPSENDKLQKELNVLKSEQNDLRLQMEAQRICLSLYYSTHVDQVR-EYMENEKDK 1153
                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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         161
                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                               13 AVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSS----LASWNYNTNITEENVQNMNNAGDK 68
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Pred. No. 1
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MISSING (IN ISOFORM 5).
STTOFHAGMER --> ALSLITSWOHHSARPTAPLFFEILSH
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VFGFYNMCFSTLC -> GSSIPELAHSDAYQTREICSS
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MISSING (IN ISOFORM 3)
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QLOEET -> LATERD (IN ISOFORM 4).
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Gaps

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RESULT 20
UTRO_HUMAN
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                                                                                                                                                                                                                                                                                                                                      STRUCTURE 7:1339-1346(1999).

STRUCTURE 7:1339-1346(1999).

FUNCTION: MAY PLAY A ROLE IN ANCHORING THE CYTOSKELETON TO THE PLASMA MEMBRANE (BY SIMILARITY TO DYSTROPHIN).

FUNCTION: NEUROMUSCULAR JUNCTION.

FUNCTION: NUCLE.

FUNCTION: MUSCLE.

SIMILARITY: STRONG, TO DYSTROPHIN.

SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY ACTIN-BINDING PROTEINS (SUCH AS ACTININ), DYSTROPHIN, FIMBRIN,
                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The 2.0-A structure of the second calponin homology domain from the actin-binding region of the dystrophin homologue utrophin."; mol. Biol. 285:1257-1264(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P46939;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Utrophin (Dystrophin-related protein 1) (DRP1) (DRP).
                                                      EMBL; X69086; CAA48829.1; -.
                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                 modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 31-256.
MEDLINE=20113481; PubMed=10647184;
MEDLINE=20113481; PubMed=10647184;
MEDLINE=20113481; PubMed=10647184;
MEDLINE=20113481; PubMed=10647184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Crystal structure of the actin-binding region of utrophin reveals head-to-tail dimer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kendrick-Jones J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS)
MEDLINE=99141377; PubMed=9887274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Primary structure of dystrophin-related protein."; Nature 360:591-593(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=93096045; PubMed=1461283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                           ABP-120, ABP-180, OR BETA-FODRIN).
SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
SIMILARITY: CONTAINS 1 WW DOMAIN REPEATS.
SIMILARITY: CONTAINS 20 SPECTRIN REPEATS.
SIMILARITY: CONTAINS 1 ZZ-TYPE ZINC FINGER.
S28381; S28381.
1BHD; 16-FEB-99.
1QAG; 01-JAN-00.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Norwood F.L.M., Moores C.A., Winder S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M., Blake D.J., Roche A., Fairbrother U., Riss J., Knight A.E., Kendrick-Jones J., Suthers G.K., Love D.R.,
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PROSITE: PS00020; ACTININ_2; 1.
PROSITE: PS50021; CH; 2.
PROSITE: PS50021; CH; 2.
PROSITE: PS50020; WW_DOMAIN_1; 1
PROSITE: PS50020; WW_DDMAIN_2; 1
PROSITE: PS01357; ZF_ZZ_1; 1.
                                                                                                                                                                 DOMAIN
ZN_FING
                                                                                   2533 LDDMNQRWNDLKAKSASIRAHLEASAEKWNRLLMSLEELIKWLNMKDEE----LKKQMPI 2588
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                2640 RNLQSKTELTPEERAQKIAKAMRKQSSEVKEK---WESLNAVTSNWQKQVDKALEKLRDL
                                                 2589 GGDVPALQLQYDHCKALRRELKEKEYSVLNAVDQARV-----FLADQPIEAPEEPR
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REPEAT
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183 YVVLKNEMARANHYEDYGDYWR--GDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHL 240
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                                                                                                    29 LDKFNHEAEDL-----FYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 79
                                                                   AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 139
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PF00397; WW;
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                                                                                                                              2.7%;
Similarity 18.5%;
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IPR001715;
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                                                                                                                                                                                                                                                                                                                                                                                           protein; Actin-binding; Calcium-binding; Cytoskeleton;
                                                                                                                                                                                                                                     1544
1652
1910
1976
                                                                                                                                                                                                                                                                       803
1016
1125
1248
1432
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPEC; 18.
TarH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spectrin; 19
                                                                                                                                                        AA;
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SPEC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZnF_ZZ; 1
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1083
1230
1334
1541
1541
1753
1753
1968
2081
2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spectrin.
TarH.
                                                                                                                                                       394488 MW; EAE8DB409F858E5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Znt_ZZ.
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                                  NEIMANSLDYNERLWAWES-----WRSEVGKQLRPLYEE
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                                                                                                                                                                                                                                                                              SPECTRIN
SPECTRIN
SPECTRIN
                                                                                                                                       Score 115.5;
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SPECTRIN
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SPECTRIN
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                                                                                                                                                                                                                                                                                                                                                                            ACTIN-BINDING.
                                                                                                                      Mismatches
                                                                                                                               No.
                                                                                                                                                                                 22.
23.
33.
34.
43.
55.
56.
77.
77.
77.
112.
113.
114.
115.
115.
116.
                                                                                                                                      DB 1;
                                                                                                                      249;
                                                                                                                      Indels 265;
                                                                                                                                     Length 3433;
                                                                                                                    Gaps
                 2696
                                                                                                                     36;
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Sear Job	Вρ	Qy	ДЪ	Qy	Db	Оу	Db	Qy	Db	Qy	рЬ	Qy	Db	Qy	Ъ	Qγ	Вb	Qy	Db
ch cor	3151	587	3097	536	3043	479	3015	428	2956	402	2904	357	2850	329	2791	297	2746	241	2697
Search completed: March 13, 2003, 16:57:36 Job time : 43 secs	YL-PVQTVLEGDNLETPITLISMWPEHYDPS 3180	YFEPLFTWLKDQNKNSFVGWSTDWSPYADQS 617	CFFSGRTAKGHKLHYPMVEYCIPTTSGEDVRDFTKVLKNKFRSKKYFAKHPRLG 315	EGPLHKCDISNSTEAGQKL-FUMLRLGKS-EPWTLALENVVGAKUMUVR-PLLN 586	HLEPQSM-VWLPVLHRVAAAETAKHQAKCNICKECPIVGFRYRSLKHFNYDVCQS 309	EMKREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKH 535	NIEPSVRSCEQQNNN		INTO-LMSLSKGLLEEKYRYLFKEVAGPTEMCDQRQLGLLLHDAIQIPRQLGEVAAFGGS 301	EAVGEIMSLSAATPKHLKSIGLLSPD 427	VPDVINCLTTTYDGLEQMHKDLVNVPLCVDMCLNWLLNVYDTGRTGKIRVQS 295	RILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFH 401	QSLADLNNVRESAYRTAIKIRRLQKALCLDLLELSTTNEIFKQHKLNQNDQILLS 290:	ENSMLTDPGNVQKAVC	RLKQLQEAHRDFGPSSQHFLSTSVQLPWQRSISHNKVPYYINHQTQTTCWDHPKMTELF- 2849	MVDQAWDAQRIEKEAEKFFVSVGL	NEKVKTVNDLSSQLSPLDLHPSLKMSRQLDDLNMR-W-KLLQVSVDD 2790	HAYVRAKIMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPEGQKPNIDVTDA 296	2697 QGAMDDLDADMKEAESVRNGWKPVGDLLIDSLQDHIEKIMAFREEIAPI 274

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                             Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_verteb::
14: sp_urclass:
15: sp_urclass:
16: sp_archeap
17: sp_archeap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        March 13, 2003, 16:53:52; Search time 36 Seconds (without alignments) 4607.442 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-978-385-2
4291
1 MSSSSWLLLSLVAVTAAQST.....ISKGENNPGFQNTDDVQTSF 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                    sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
              sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                        sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                         sp_invertebrate:*
sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB	ength	8	ID	Description
1	4291	100.0	805	4	Q9NRA7	O9nra7 homo sapien
2	4288	99.9	805	4	Q9BYF1	0
ω	4281	99.8	804	4	Q9UFZ6	homo
4	3579	83.4	805	_	Q8R0I0) mus
ъ	3485	81.2	798	11	Q99N71	
o	1539	35.9	353	,-	Q99N70	099n70 mus musculu
7	1336	31.1	732	σ	Q9GLN6	Q9qln6 pan troqlod
8	1329	31.0	1304	σ	Q9GLN7	09gln7 pan troglod
9	1310	30.5	1313	11	Q9EQM9	Q9eqm9 rattus norv
10	1303	30.4	694	4	Q15540	Q15540 homo sapien
11	1089.5	25.4	648	ഗ	Q9NDS8	Q9nds8 bombyx mori
12	1086	25.3	615	υī	Q9NKE4	Q9nke4 drosophila
13	1057	24.6	660	G	Q17248	
14	1030	24.0	630	u	Q24222	Q24222 drosophila
15	1028	24.0	630	ഗ	Q9VLJ6	09vlj6 drosophila
15	1004	ر 2	249	_	090836	

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11011 10011	21.7 19.6 15.0
500 501 602 602 602 602 602 602 602 602 602 603 604 604 604 605 606 606 606 606 606 606 606 606 606	844 792 907
55 55 55 55 55 55 55 55 55 55 55 55 55	រាបាលបា
09VJV20 09VJV20 09VJV20 064603 09ESG4 09ESG4 09ESG4 09BDG1 016425 0116425 0116425 09TX66 09TX	Q8SXX2 Q9VJV1 Q18581
Oyviz drosophila Oyviz drosophila O9viyz drosophila O64603 rattus norv O9w0z1 drosophila O9su59 drosophila O9su59 drosophila O9seg4 mus musculu O9bdg1 bos taurus O1425 homo sapien O61265 mus musculu O9tx66 drosophila O9kfv0 bacillus ha O8kfv0 bacillus ha O8y616 listeria mo O9nke3 drosophila O95161 canis famil O92ac3 listeria in O8yw66 anbaena sp O9pw8 ureaplasma O9pw8 ureaplasma O9pw8 ureaplasma O9si52 enterococcu O9sl27 arabidopsis O9xy8 dictyosteli O8r670 fusobacteri O81636 mus musculu	

ALIGNMENTS

KΨ	אַ אָ	DR	DR	DR	DR	DR	DR	DR	RL	RΤ	RT	RA	RA	RA	RP	RN	RL	RT	RT	RA	RA	RC	RP	RN	ò	8	8	20	DE	DE	DΤ	ŊΤ	DŢ	AC	IJ	RESULT Q9NRA7
ptidase.	PROSITE: PS00142: ZINC PROTEASE; UNKNOWN 1.	PROU791; PEPDIPTASEA.	Pfam; PF01401; Peptidase_M2; 1.	InterPro; IPR000130; Zn_MTpeptdse.	548;	ľ	EMBL; AF291820; AAF99721.1;		Circ. Res. 0:0-0(2000).		"A novel ACE-related carboxypeptidase (ACE2) converts angiotensin I to	S.;	M., Woolf B., Robison K., Jeyasee		SEQUENCE FROM N.A.		Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.	on Ās A Captopril-Insensitive Carboxypept	"A Human Homolog of Angiotensin Converting Enzyme - Cloning and		Tipnis S.R., Hooper N.M., Hyde R.J., Christie G., Karran E.,	TISSUE=LYMPHOMA;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=9606;	Primates; Catarrhin:	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	idase ACE2)	enzym	(TrEMBLrel. 19, Last annotation	(TrEMBLrel. 15,	2000 (TrEMBLrel.	~ .	Q9NRA7 PRELIMINARY; PRT; 805 AA.	ILT 1 PA7

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Matches
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Q9BYF1;
01-JUN-2001
01-JUN-2001
01-JUN-2002
                  ACE2.
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   sapiens
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Submitted (APR-2001) to the
EMBL; AB046569; BAB40370.1;
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InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 1.
PRINTS; PR00791; PEPDIPTASEA.
PROSTITE; PS00142; ZINC_PROTEASE; UNKNOWN_1
PROSTITE; PS00142; ZINC_PROTEASE; UNKNOWN_1
SEQUENCE 805 AA; 92491 MW; D2AAB4C27081
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                                                                                                                                                                                                                                                                                                                                   NMNNAGDKWSAFIKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL
                                                     NSFVGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKN
                                                                                                                             KCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK
                                                                                                                                                                                    KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
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                                  NSFYGWSTDWSPYADQSIKVRISLKSALGDRAYEWNDNEMYLFRSSVAYAMRQYFLKVKN
                                                                                                           KCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK
                                                                                                                                                                                                                                                                                                                                                                                                              AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM
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the EMBL/GenBank/DDBJ
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Pred. No. 5.8e-305;
1; Mismatches 0;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 92.3 kDa protein (Fragment).
DKFZP434A014.
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EMBL; AL110224; CAB53882.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 1.
PRINTS; PR00791; PEPDIPTASEA.
ProDom; PD004184; Peptidase_M2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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                                                                                                                                                                                                        121 TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 180
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                                                                                                                                                                                                                                                                                  62 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 121
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                                                                                                                                                    AYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 301
                       TKYTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 421
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                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                            99.8%; Score 4281; DB 4; 99.9%; Pred. No. 1.9e-304;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
RIKEN cDNA 2010305L05 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC026801; AAH26801.1; .
SEQUENCE 805 AA; 92367 MW; D8B883AAC966A8D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8R0I0;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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                 241 HAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQ 300
                                                                                                                  121 NTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY 180
 241
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                                                                                                                                                                                                                                    1 MSSSSWLLLSLVAVTAAOSTIEEQAKTELDKENHEAEDLEYQSSLASWNYNTNITEENVQ 60
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                                                                                                      NTMSTIYSTGKVCNPKNPQECLLLEPGLDEIMATSTDYNSRLWAWEGWRAEVGKQLRPLY 180
                                                                                                                                                         KMSEAAAKWSAFYEEQSKTAQSFSLQEIQTPIIKRQLQALQQSGSSALSADKNKQLNTIL 120
EEYVVLKNEMARANNYNDYGDYWRGDYEAEGADGYNYNRNOLIEDVERTFAEIKFLYEHL
                                                                           EEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGOLIEDVEHTFEEIKPLYEHL
                                                                                                                                                                                                                                                                 661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                             83.4%; Score 3579; DB 11; Length 805; 82.1%; Pred. No. 4.2e-253;
                                                                                                                                                                                                                                                                    60; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     805 AA.
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                            Query Match
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      Best Local Similarity
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                                                         Carboxypeptidase.
SEQUENCE 798 AP
                                                                          PRINTS; PRO0791; PEPDIPTASEA.

PRODOM; PD004184; Peptidase_M2; 1.

PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                    Komatsu T., Sugano S., Imai J., Suzuki Y., Hanaoka K., Ymada Y., Hida M., Tanigami A., Muroi S.;
"Molecular cloning, mRNA expression, and chromosomal localization of mouse Angiotensin-converting Enzyme-Related Carboxypeptidase.", Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. "BBBLS: AB053181; BAB40431.1; -.
                                                                                                                                              Pfam; PF01401; Peptidase_M2;
                                                                                                                                                          InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                         MGD; MGI:1917258; 2010305L05Rik.
InterPro; IPR001548; Peptidase_M2.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                     2010305L05RIK OR ACE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           781 YDSMDIGKGESNAGFQNSDDAQTSF 805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 KCDISNSTEAGOKLENMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDONK 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QMILFGEEDVRVANLKPRISFNFFVTAPKNVSDIJPRTEVEKAIRMSRSRINDAFRLNDN 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSFVGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTVPFLEEDVRVSDLKPRVSFYFFVTSPQNVSDVIPRSEVEDAIRMSRGRINDVFGLNDN 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSFYGWNTEWSPYADQSIKVRISLKSALGANAYEWTNNEMFLFRSSVAYAMRKYFSIIKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH 540
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                                                      798 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                 91943 MW;
      81.2%;
82.2%;
Score 3485; DB 11; Pred. No. 3.1e-246;
                                            403AEA29D55725A4 CRC64;
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             Length 798;
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                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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        NCBI_TaxID=10090;
                                                          Mus musculus (Mouse)
                                                                               Anigotensin-converting enzyme-related carboxypeptidase.
                                                                                                                                                                               Q99N70
                                                                                                                                                              Q99N70;
                                                                                                                                                                                                                                                                                                              721 SLEFLGIHPTLEPPYOPPYTIWLIIFGVVMALVVVGIIILIVTGIKGRKKKNETKREESP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 CTKVTMDNFLTAHHEMGHIQYDMAYARQPFLLRNGANEGFHEAVGEINSLSAATPKHLKS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 GWDAERIFQEAEKFFVSVGLPHMTQGFWANSMLTEPADGRKVVCHPTAWDLGHGDERIKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 AWDAORIFKEAEKFFYSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDERILM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 HAYVRRKLMDTYPSYISPTGCLPAHLLGDMWGRFWTNLYPLTVPFAQKPNIDVTDAMMNQ
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                                                                                                                                                                                                                                                              YDS 783
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                                                                                                                                                                                                                                                                                                                                                                             QTVPFLEEDVRVSDLKPRVSFYFFVTSPQNVSDVIPRSEVEDAIRMSRGRINDVFGLNDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KMSEAAAKWSAFYEEQSKTAQSFSLQEIQTPIIKRQLQALQQSGSSALSADKNKQLNTIL
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                                                                                                                                                                          PRELIMINARY;
            Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Komatsu T., Sugano S., Suzuki Y., Hnaoka K., Yamada Y.; "Molecular cloning of ACE2."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AB053102; BAB40432.1; -. MEROPS; M02.006; -:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Komatsu T., Sugano S., Imai J., Suzuki Y., Hanaoka K., Ymada Y., Hida M., Tanigami A., Muroi S.; "Molecular cloning, mRNA expression, and chromosomal localization of mouse Angiotensin-converting Enzyme-Related Carboxypeptidase."; submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01401; Peptidase_M2; 1.
PRINTS; PR00791; PEPDIPTASEA.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carboxypeptidase
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InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                          O9GLN6:
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Dipeptidyl carboxy peptidase 1 testicular form.
"Human-Chimpanzee DNA sequence variation in the four major genes of the renin angiotensin system."; genomics 69:14-26(2000).
EMBL; AF193486; AAG31359.1; JOINED.
                                                                                                                                                                                Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa; Chordata; Craniata; Verlebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                           Q9GLN6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                Dufour C., Casane D., Denton D., Wickings J., Corvol
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                               NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                           301
                                                                               Jeunemaitre X.;
                                                                                                              MEDLINE=20469400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTMSTTYSTGKYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSSSSWLLLSLVAVTTAQSLTEENAKTFLNNFNQEAEDLSYQSSLASWNYNTNITEENAQ 60
                                                                                                                                                                                                                                                                                                                                                                                                         AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEYVYLKNEMARANNYNDYGDYWRGDYEAEGADGYNYNENQLIEDVERTFAEIKPLYEHL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KMSEAAAKWSAFYEEQSKTAQSFSLQEIQTPIIKRQLQALQQSGSSALSADKNKQLNTIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEYYVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTMSTIYSTGKYCNPKNPQECLLLEPGLDEIMATSTDYNSRLWAWESWRAEVGKQLRPLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 AA; 40442 MW; D17B71141EE4AF5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 22; Mismatches 44;
                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                 PubMed=11013071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.9%;
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                                                                                                                                                                                                                                                                                                                                732 AA
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Q9GLN7;

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 1
PRINTS; PR00791; PEPDIPTASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probom; PD004184; Peptidase_M2; 1.
Probom; PD004184; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 732 AA; 83428 MW; C43D06443A47E74B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                          302 WDAORIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILM 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                   183
                                                                                                                                                                               461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 TAAQS----TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNM 62
                                                                                     541 KCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TSAQSPULVTDEAEASKFVEEYDRTSQVVWNEYAEANWUYUTUITTETSKILLQKUMQIA 120
640 LHGEKLGWPQYNWTPNSARS 659
                          601 --NSFVGW-STDWSPYADQS 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF193474;
AF193475;
AF193476;
                                                                                                                                                                                                                                                                                                                                                                                      YVRAKLMNAY-PSYISPIGCLPAHLLGDMWGREWTNLYSLTVPFGQKENIDVTDAMVDQA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METTYSVATVCHTNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF193479;
AF193480;
AF193481;
                                                                                                                                                                                                                                                                                                                                                                                                                     YVELINQAARLNGYVDAGDSWRSMYETPSLE-----QDLERLFQELQPLYLNLHA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                               YVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHA 242
                                                                                                                                            KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYTTRTLYQFQFQEALCQAAKHEGPLH 540
                                                                                                                                                                              LNLLSSEGGSD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSL 519
                                                                                                                                                                                                                                       CTTVNLEDLVVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHS
                                                                                                                                                                                                                                                                 CTKYTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
                                                                                                                                                                                                                                                                                                 WTPRRMFKEADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQ 400
                                                                                                                                                                                                                                                                                                                                                            YVRRALHRHYGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQG
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                                                        KCDIYQSKEAGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENE
                                                                                                                   RLKYQGLCPPVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLH
                                                                                                                                                                                                          IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LKYGTQARRFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG31359.1;
AAG31359.1;
AAG31359.1;
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AAG31359.1;
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AAG31359.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205;
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PRINTS; PR00791; PEPDIPTASEA.
PRODOM; PD004184; Peptidase_M2; 2.
PROSITE; PS00142; ZINC_PROTEASE; U
252 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKE 310
                                                                                      132 VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYYVLKNEMA 191
                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                            696 --LKYGTQARREDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVAT 753
                                                                                                                                                        642 TDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIANHT-----
                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                      InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Euthería; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                  72 FIKEQSTLAQMYPLQEIQNLTYKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK 131
                                                                                                                                                                     Genomics 69:14-26(2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the renin angiotensin system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Human-Chimpanzee DNA sequence variation in the four major genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20469400; PubMed=11013071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan troglodytes (Chimpanzee).
Eukarvota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dipeptidyl carboxy peptidase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jeunemaitre X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9598;
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                      RLNGYVDAGDSWRSMYETPSLE------QDLERLFQELQPLYLNLHAYVRRALHRH 861
                                           RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 251
                                                                 VCHTNG---SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA 811
                                                                                                                                                                                                           254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF193472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF193486; AAG31358.1;
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                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ., Casane D., Denton D., Wickings J., Corvol
                                                                                                                                                                                                                                                    1304 AA;
                                                                                                                                                                                                           Conservative
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AAG31358
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                                                                                                                                                                                                                   31.0%; Score 1329; DB 6; Length 1304; 41.6%; Pred. No. 3.3e-88;
                                                                                                                                                                                                                                                149369 MW; DCF728D0BA0F1314 CRC64;
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                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                              UNKNOWN_1.
                                                                                                                                                                                                                 No.
                                                                                                                                                                                                                  3.3e-88;
                                                                                                                                                                                                      205;
                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001348; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 2.
PRINTS; PR00791; PEPDIPTASEA.
ProDom; PD004184; Peptidase_M2; 2.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 1313 AA; 150941 MW; E888341562542B04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jafarian-Tehrani M., Listwak S., Barrientos R.M., Michaud A., Corvol P., Sternberg E.M.; "Characterization of a missense mutation in the angiotensin I-converting enzyme cDNA in exudative inflammation resistant F344/N
       140 ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDY 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF201331; AAG35596.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-F344/N; TISSUE=LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                           710 AKTFDVSNFQNSTIKRIIKKVQNVDRAVLPPNELEEYNQILLDMETTYSVANVCYTNG-- 767
                                                                                                                                                                                                                        650 TDEAKANREVEEYDRTAKVLWNEYAEANWHYNTNITIEGSKILLQKNKEVSNHTLKYGTW 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiotensin-converting enzyme.
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                                                                                                                                                80 AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 139
                                                                                                                                                                                                                                                                 20 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITTEENVQNMNNAGDKWSAFLKEQSTL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1042 SD-EHDINFLMKNALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         922 ADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     862 YGAQHINLEGPIPAHLLGNNWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE
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                                                                                                                                                                                                                                                                                                                                                                                              251;
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                                                                                                                                                                                                                                                                                                                                                                                                                     h 30.5%; Score 1310; DB 11; Similarity 42.0%; Pred. No. 8.1e-87;
                                                                                                                                                                                                                                                                                                                                                                        Conservative 115; Mismatches 214; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1313;
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01-NOV-1996
01-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1177 MKLGYSKOWPEAMKIITGOPNMSASAIMNYFKPLTEWLVTENRRHGETLGWPEYTWTP 1234
                                                                                                                                                                                                                                                                                                                                           angiotensin-converting enzyme.";
proc. Natl. Acad. Sci. U.S.A. 86:7741-7745(1989).
EMBL; M26658; AAA60612.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q15540
                                                                                                                                                                                                                                                                                                                                                                                                   Ehlers M.R., Fox E.A., Strydom D.J., Riordan J.F.;
"Molecular cloning of human testicular angiotensin-converting enzyme:
the testis isozyme is identical to the C-terminal half of endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259
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                                                                                                                                                                                                                                      PTam; PF01401; Peptidase_M2; 1.
PRINTS; PR00791; PEPDIPTASEA.
PRODOM; PD004184; Peptidase_M2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       558 LRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                498
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                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90046671; PubMed=2554286;
                                                                                                                                                                                                                                                                                                         InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
109 IKKVQDLERAALPAQELEEYNKILLDMETTYSVATVCHPNG--SCLQLEPDLTNVMATSR 166
                                  97
                                                                      57
                                                                                                       45 LASWNYNTNITEE-----NVQNMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQ 96
                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDSWRSSYESDDLE-----QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCLSLEPDLTNIMATSRKYEELLWVWKSWRDKVGRAILPFFPKYVDFSNKIAKLNGYSDA 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGPIPAHLLGNMWAQTWSNIYDLVAPFPSAPSIDATEAMIKQGWTPRRIFKEADNFFTSL 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FDPGSKFHVPANVPYIRYFISFIIQFQFHEALCRAAGHTGPLYKCDIYQSKEAGKLLADA 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLMKMALDKIAFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGD 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETY 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIQYFMQYKDLPVTFREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSE-GSGYEHDIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTSVNMEELVIAHHEMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein.
                                LQALQQNGSSYLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSL 156
                                                                      IATKNYNTNITTETSKILLQKNMQIANHT-----LKYGTQARKFDVNQLQNTTIKRI 108
                                                                                                                                                                                                                    694 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                               Conservative
                                                                                                                                                                                                                    79333 MW;
                                                                                                                                                                 30.4%; Score 1303; DB 4; Length 694; 42.7%; Pred. No. 1e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Strydom D.J., Riordan J.F.;
                                                                                                                                                 107; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                      57C0FF9C5AECA119 CRC64;
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                                                                                                                                            InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 1.
PRINTS; PR00791; PEPDIPTASEA.
PRODOm; PD004184; Peptidase_M2; 1.
PROSITE; PS00142; ZINC_PROTERSE; UNK SEQUENCE 648 AA; 74917 MW; 9A740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9NDS8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ecdysteroid-inducible angiotensin-converting enzyme-related gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 DYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYD 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bombyx mori (Silk moth)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000
                                                                                                                                                                                                                                                                                    EMBL; AB026110; BAA97657.1;
                                                                                                                                                                                                                                                                                                       converting enzyme-related gene in wing discs of Bombyx morinsect Biochem. Mol. Biol. 31:97-103(2001).
                                                                                                                                                                                                                                                                                                                                    "Isolation and expression of the ecdysteroid-inducible angiotensin-
                                                                                                                                                                                                                                                                                                                                                       Kanke E., Kawasaki H.;
                                                                                                                                                                                                                                                                                                                                                                        Quan G.X., Mita K.,
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C108; TISSUE-WING IMAGINAL DISK; MEDLINE=20556050; PubMed=11102839;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bombycoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    575 GAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSPYADQS 617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337
                                                                                                                                                                                                                                                                 MEROPS; M02.002;
                                                                                                                                                                                                                                                                                                   Insect Biochem. Mol. Biol.
                                   11 LVAVTAAQSTIEEQAK-TFLDKFNHEAEDLFY------QSSLASWNYNTNITEEN 58
10 LIAAIVAVFIVATQGRDPDLEAREHEAREYMLHLDKATGLRKNRASLAEWEYTSNITKEN 69
                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KYEDLLWAWEGWRDKAGRAILOFYPKYVELINQAARLNGYVDAGDSWRSMYETPSLE--- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKEADDFFTSLGLLPVPPEFWNKSMLEK 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY-PSYISPIGCLPAHLLGDMWGRFW 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THLYSLTVPFGQKPHIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLPHMTQGFWENSMLTD 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWPQYNWTPNSARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKEAGQRLATAMKLGFSRPWPEAMQLIT 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRTQGDFDPGAKFHIPSSVPYIR 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHVSNDYSFIR 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGGSD-EHDINFLMKMALDKIAFIPFSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLLKQALTIVGTLPFTY 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTDGREVVCHASAMDFYNGKDFRIKQCTTVNLEDLVVAHHEMGHIQYFMQYKDLPVALRE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRN 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YYTRTLYOPOFQEALCOAAKHEGPLHKCDISNSTEAGOKLFNMLRLGKSEPWTLALENVV 574
                                                                        232;
                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -QDLERLFQELQPLYLNLHAYVRRALHRHYGAQHINLEGPIPAHLLGNMWAQTW 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                            Okano K., Shimada T., Ugajin N., Xia Z., Goto N.
                                                                                           25.4%; score 1089.5; 35.6%; Pred. No. 3.96
                                                                                                                                                 9A740AA9FCACEBF0 CRC64;
                                                                            Mismatches
                                                                                                                                                                    UNKNOWN_1
                                                                                         No. 3.9e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      648
                                                                                                              DB 5; Length 648;
                                                                                259;
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             621
                                                                                35;
                                                                                Gaps
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ACCOMPAGNOS ACCOMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
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Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
                                                                                                                                                                                                                        Celniker S., Rubin G.M.; "An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.";
                                                                                           STRAIN-BERKELEY,
                                                                                                                                                                                                                                                                                                                           Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                         Genetics 153:179-219(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99403001; PubMed=10471707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ance protein (LD11258p). ANCE OR CG8827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9NKE4; Q9VJV3;
01-OCT-2000 (Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9NKE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       598 PLHDWLRAENQRTGEHIGWEPTNMEYCTPSQLSELNVKEPSSSPATQQSDS 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           590 PLFTWLKDONKNS--FVGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDN 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   538 HAAGDPNKKLVDCDIYQSVAAGNALANMLKMGSSKPWPDAMEALTGQREMKADGLLEYFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    535 HEG-----PLHKCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFE 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478 HYWKLREQLQGVEPPVNRTEDDFDAAAKYHVSSNVEYARYYVSFIIQFQFHRGVCQLAGE 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         476 KWWEMKREIVGYVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQ-AAK 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 PLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLY 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 KNFTDYVNLYNEAAKLNGFDNVAEWWQSEYEVPDFE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 TVSGMESNYATAKICSYKNESKCDLSLEPEITEIFSTSQDPEELKHAWVEWHNAAGATAK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KHLRRVGLATGD-AEDEQTEINQLYKMGIDKIAFLPFAYTLDLFRYGVFRRKTLPEDYNC 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KHLKSIGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRIKQCTTVDYEYFQTTHHEMGHIQYYLQYRDQPVVFRDGANQGFHEAVGDTIALSVSSP 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATP 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRDQNYTPMKMFQMSDEFFRSLNLTAMPEKFWKNSIIEKPTD-REIVCHASAWDFFDGED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MVDQAWDAQRIFKEAEKFEVSVGLPNNTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-D 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQLHAYVRKRLRDKYGDKVVSARGPIPAHLLGNMWAQTWNNIESFTRPYPDKKEIDVTQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EHLHAYVRAKLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQNMNNAGDKWSAFIKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILNTMSTIYSTGKVCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEKSIQTHLELSRQEKAAWEETKMYGWQDFQDFTLRRMFKKYSQLGVAALPDDKFQALMR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       615 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----EQLAKLWEDVKPLY 239
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RA Abril J.F., Agbayani A., An H.-J., Andrews-pfannkoch C., R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Borkova D., Botchan M.R., Bouck J., Banndari D., Bolshakov S., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Bockova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botcher R., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harrey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harrey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harrey D., Heiman T.J., Hernandez J.R., Houck J., RA Liu X., Mattel B., McIntosh T.C., Kravitz S., Kulp D., Lai Z., RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Nalson K.R., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Ra Wang Z.-Y., Wassarman D.A., Weinstook G.M., Weissenbach J., Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Wang Z.-Y., Scheele T., Zhong W., Shong G., Zhao Q.A., Zheng L., Rab Gibbs R.A., Myers E.W., Rubi G.M., Venter F., Shen Y., Sheng L., Rab Gibbs R.A., Myers E.W., Rubi G.M., Venter T., Sheng L., Rab Gibbs R.A., Nyers E.W., Rubi G.M., Venter T., Sheng L., Smith H.O., Rab Gibbs R.A., Weissenbach J., Sheng L., Rab Gibbs R.A
                                      Query Match
                                                                                                  Pfam; PF01401; Peptidase_M2; 1.
PRINTS; PR00791; PEPDIPTASEA.
PRODOM; PD004184; Peptidase_M2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                          Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003408; AAF44834.1; -.

EMBL; AE003641; AAF53353.2; -.

EMBL; AY061129; AAL28677.1; -.

FlyBase; FBgn0012037; Ance.
                                                                                                                                                                                                               InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
Zieran L.L., Rubin G.M.;
     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                       615 AA;
                                                                                       70913
25.3%; Score 1086; DB 5; 36.4%; Pred. No. 6.4e-71;
                                                                                    WW;
                                                                            9E3691BCC51D6C48 CRC64;
                     Length 615;
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Matches

Conservative

122;

Mismatches

Indels

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Q17248
ID Q1724
AC Q1724
DT Q1-NO
DT 01-NO
DT 01-NO
DT 01-NO
DT 01-W
DE Angio
GN BM91.
OS BOOPH
OC PATAS
OC PATAS
OC PATAS
OC NCBI_
RN [1]
RP SEQUE
RA BHOWN
RT TICH
RA BLOWN
RT TICH
RA SUDMI
DR PFEM;
DR PRINT
DR PFEM;
DR SIGNA
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01-NOV-1996
01-JUN-2002
                                                                                                         Whitfeld P.L., Johnson M.C., Smith D.R.J., Sne Brown G.S., Cairns D., Foy A.B., Irving D.O.; "The Cloning of an Angiotensin-Converting Enzy Tick Boophilus microplus."; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ EMBL; U62809, AAB0498.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q17248
Q17248;
ProDom; PD004184;
Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                               Boophilus microplus (Cattle tick).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida;
Parasitiformes; Ixodida; Ixodidae; Boophilus.
                                                                                                                                                                                                        SEQUENCE FROM N.A. Whitfeld P.L., Joh
                                                                                                                                                                                                                                                                                                                                                       01.NOV-1996 (TrEMBLrel. 01, Created)
01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01.NOV-1996 (TrEMBLrel. 21, Last annotation update)
Angiotensin-converting enzyme-like protein precursor
                                                        PRINTS;
                                                          Pfam; PF01401; Peptidase_M2; 1. PRINTS; PR00791; PEPDIPTASEA.
                                                                                                                                                                                                                                                             NCBI_TaxID=6941;
                                                                                             InterPro; IPR001548; Peptidase_M2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLG-KGDFRILMCTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLRKHYGDAVVSETGPIPMHLLGNMWAQQWSEIADIVSPFPEKPLVDVSAEMEKQGYTPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STGKVCNPDNPQEC-LLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELAKFMKEVASDTTKFQWRSYQSEDLKRQFKALTKLGYAALPEDDYAELLDTLSAMESNF 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K-DYVRDDEARINQLFLTALDKIVFLPFAFTMDKYRWSLFRGEVDKANWNCAFWKLRDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KMFQMGDDFFTSMNLTKLPQDFWDKSIIEKPTDGRDLVCHASAWDFYLTDDVRIKQCTRV
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                                     Peptidase_M2; 1.
   POTENTIAL
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                                                                                                                                  databases
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Best Local
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SEQUENCE FROM N.A.
MEDILINE-971128790; PubMed-8973330;
MEDILINE-971128790; PubMed-8973330;
MEDILINE-971128790; PubMed-8973330;
MEDILINE-97128790; PubMed-897330;
MEDILINE-97128790; PubMed-897330;
MEDILINE-97128790; PubMed-897330;
MEDILINE-97128790; PubMed-897330;
MEDILINE-97128790; PubMed-897330;
MEDILINE-97128790; PubMed-897300;
MEDILINE-97128790; PubMed-897300;
MEDILINE-97128790; PubMed-897300;
ME
                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
METALLOPEPTIDASE (Angiotensin-converting enzyme-r
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EMBL; X96913; CAA65632.1; -
EMBL; X96913; CAA656
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InterPro; IPR000130; Zn_MTpeptdse.
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QE--NSRLGVPLGWGP 616
                                                                               DQNKNSFVGWSTDWSP 612
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                                                                                                                                                                                                                                 --LHKCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLK 596
                                                                                                                                                                                                                                                                                                                          efggveppvfrtekdfdppakyhidadveylryfaahifqfqfhkvlcrkagqyapnnsr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFRLRQHYGPDVMPAEGNIPISLLGNMWGQSWNELLDLFTPYPEKPFVDVKAEMEKQGYT
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PD004184; Peptidase_M2; 1.

PD00412; ZINC_PROTEASE; UNKNOWN_1.

PS00142; ZINC_PROTEASE, UNKNOWN_1.

PS00143; PS0014
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havez C., Chew M.,
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Golle R.F., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Golle R.F., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Golle R.F., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Golle R.F., RA Adams M.D., Celniker S.E., Richards S., Ashburner M.A., Henderson S.N., RA Brandon R.C., Robers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D., RA Brandon R.C., Royaland A., An H.-J., Andrews Pfennkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Becson K.F., Bence P.V., Berman B.P., Bhandari D., Botshakov S., RA Borkvoa D., Botchen M.R., Bouck J., Brokstein P., Brottier P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Downes M., Duyan Rocha S., Dunkov B.C., Dunn P., RA Cherry J.M., Evangellsta C.C., Ferraz C., Ferriera S., Fleischmann W., Statis R.J., House J., House J
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Q9VLJ6
ID Q9VLJ
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01-MAY-2000 (TrEMBLrel. 13, C

01-MAY-2000 (TrEMBLrel. 13, I

01-DEC-2001 (TrEMBLrel. 19, I

ACER protein (LD28328P)

ACER OR CG10593
                                                                                                         Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan R., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003621; AAF52693.1; -.
InterPro; IPR001548; Peptidase_M2.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 1.
                                                                   FlyBase; FBgn0016122; Acer
                                                                                         MEROPS; M02.002;
                                                                                                                                                                                                                                                                                       STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                     Q9D836 PRELIMINARY;
Q9D836;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
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ProDom;
PROSITE;
                                                   SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-SMALL INTESTINE;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                              Kawai J.,
                                                                                                                                                                                                                                                         2010305L05Rik protein 
2010305L05RIK.
                                                                                                                                                          NCBI_TaxID=10090;
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219; Conserv
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PD004184; Peptidase_x
PS00142; ZINC_PROTEA
                                 Shinagawa A.,
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35.6%;
     Fukunishi Y., Konno H.,
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Shibata K., Yoshino M., Itoh M. kunishi Y., Konno H., Adachi J.,
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Last sequence update)
Last annotation updat
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Pred. No. 1
                                                                                                                                                                          Craniata; Vertebrata;
Sciurognathi; Muridae;
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Mismatches
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                                                                                                                                                                               Muridae;
                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                        Euteleostomi;
                         Ι.
                                                                                                                                                                               Murinae;
       Fukuda
                              Ishii
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Best Local
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Q8SXX2;
Q1-JUN-2002
Q1-JUN-2002
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                    Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawez C., Dorsett V., Dresnek D., Frise George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.
                                                                                                                                          STRAIN=BERKELEY;
Stapleton M., Brokstein P.,
                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Merazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyos
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:1917258; 2010305L05Rik.
InterPro; IPR001548; Peptidase_M2.
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(TrEMBLrel.)
(TrEMBLrel.)
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AA; 28379 MW
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashurner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, CG17988 protein.
                                                                                                                                                                              STRAIN-BERKELEY;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Pterygota; Neoptera; Endopterygota; Diptera Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Trac
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                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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A Mount S.M., Moy M., Murphy B., Murphy L.M., Muzny D.M., Nelson D.L.,
A Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Pollard W., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
A Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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Best Local
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Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Bockova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun
Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Book B., Bellian A.E., Garg N.S., Gelbart W.H., Houck J.,
Book B., Bo
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PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 792 AA; 92321 MW; 757EC472089022B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001548; Peptidase_M2;
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01401; Peptidase_M2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.,
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FlyBase; FBgn0032536; Ance-3.
506
                                                                                     346
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                                                                                 PTAWDL-GKGDFRILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAV
                                                                                                                                                                                                                                                                                                                                                                 DIVWEQIRPLYEGLHAYVRRKLRDYYGPDRINRIAPIPSHILGNMYGQSWSNVLDILIPY
                                                                                                                                                                                                                                                                                                                                                                                                            YNYNNNPNVEFV-GINNRNRFENPFLSNQDRFNLNQGYLERQRYQQDRRYQQELEKLRIL
PSAWDFCNRHDFRVKICTDINQRSLISVHHEMAHIQYFLQYRHLPKIFRNGANPAFHQAV
                                                                                                                                                                                PGRKLIDVTPRMVEQGYTPQLMFQLAEEFFTSINMSAVGPEFYRNSIFEQPLD-RRVLCE
                                                                                                                                                                                                                                GQKPNIDYTDAMYDQAWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----PLQEIQNLTVK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beasley E.M.,
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Pfam; Pf01401; Peptidase_M2; 1.
ProDom; PD0041104; Peptidase_M2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=BRISTOL N2; MEDLINE=99069613;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                          Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases EMBL; U56966; AAA98719.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                                                                                                                                      Waterston R.;
                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                    Hallsworth K.;
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
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                                                                                                                                                                                 Local
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ALNRDSKDSTICDKDVPPPCALQKIDMDSIFRNEKDASRLQHLWVSYVTAIAKS-KPSYN
                                                                               MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN
                                                                                                         SSNYWKTDNLQAPGSIKD--EEKLRSWLAGYEAEAIKVLREVALSGWRYFNDASPSLKLA
                                                                                                                                    SSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQN
                         TMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE
                                                   LDEAENVLTMFVRSTSMQAKQFDMASVTDEKVMRQLGYVSFEGMSALAPSRFADYSQAQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IYRGLCRESGQYVPGDPRKPLHQCDIYRQPAAGNILKTLMSKGASQPWQEVLEETLREGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGNANKRIMNCHYWN------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDAIGLSVSTPRHLQTLGLLQRSLDE-SSYDINYLFTMAIDKVAFLPFALSLDNWRYDVF 624
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                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                     Submission.";
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907 AA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                              Score 642.5; DB 5
Pred. No. 3.1e-38;
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barndon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barndon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barndon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barndon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barndon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
RA Genablos B., Cawley S., Dahlke C., Davenort L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenort L.B., Davies P.,
RA Genablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Posler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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ANCE-4 OR CG8196.
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pullard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
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PRINTS; PR00791; PEPDIFTASEA.
Probom; PD004184; Peptidase_M2; 1.
SEQUENCE 661 AA; 76218 MW; 2C8
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InterPro; IPR001548; Peptidase_M2
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GKILPNNTGLSSLALLEYYQPVLDWLNKYNKDANSKIGWTA-----SKKMVVT----
                                                                                                               YYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLGKSEPWTLALENVV 574
                                                                                                                                                                            HTKVMHDLLNDTVDMDTVNKHYWRLMEQHAGIEAPSDRSEGAIDFPYKFYVNIDQSFQTQ
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134; Mismatches 303; Indels 103;
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Search completed: March 13, 2003, 16:58:02 Job time: 46 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
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                                                      Sequence 5, Appli
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Sequence 4028, Ap	Sequence 2/, Appr	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli		Sequence 2, Appri	22,	u L	ر ا ا	•		Sequence 3, Appri	, L	sequence 2, Appri	α4	L L	13, 2

ALIGNMENTS

RESULT 1 US-08-989-299-2

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; Sequence 2, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
APPLICANT: Robinson, Keith E.
APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
QΥ
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                                                                      QΥ
                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-989-299-2
                                                                                                                  Matches 805;
                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 805 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: MIJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEPAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: N
                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Arnold E., Beth REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/989,299
                                                                                                                                                                                                                              TOPOLOGY:
61 NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
                                                        MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60
                                    MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60
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Pred. No. 0;
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US-08-481-626-2
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                                                                                                                                          APPLICANT: Hubert, Christine
APPLICANT: CORVOL, Pierre
TITLE OF INVENTION: Nucleic Ac.
TITLE OF INVENTION: Testicular
TITLE OF INVENTION: Enzyme in NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              APPLICANT:
                                                  STREET: 1300 I S
CITY: Washington
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                                      STATE:
                                                                                      ADDRESSEE: Finnegan, Henderson, Farabow, ADDRESSEE: Dunner
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                                                                   E: Dunner
1300 I Street,
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                                                                     N.W.,
                                                                       Suite 700
                                                                                                        Garrett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meyers, Kenneth J. 16 REGISTRATION NUMBER: 25,146 REFERENCE/DOCKET NUMBER: 045 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
         541
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                                                                                                          461 LNILSSEGGSD-EHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 05-JUL-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NHT-----LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 TAAQS----TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE------NVQNM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 NNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TSAQSPNLVTDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIA 120
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STRANDEDNESS: sir
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KCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK 600
                                  RLKYQGLCPPVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLH
                                                         KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
                                                                                                                                            IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM
                                                                                                                                                                                 CTTVNLEDLVVAHHEMGHIQYFMQYKDLPVALREGANPGFHEAIGDVLALSVSTPKHLHS
                                                                                                                                                                                                                    CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS
                                                                                                                                                                                                                                                         WTPRRMFKEADDFFTSLGLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQ
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                                                                                                                                                                                                                                                                                                                                  YVRRALHRHYGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METTYSVATVCHPNG---SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259;
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41.8%; Pred. No. 4.8e-120;
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APPLICANT: Robinson, Keith E.

TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                              173 METTYSVATVCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPK 230
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                                                                                                                       183 YVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: MIZ-
TLECOMMUNICATION TO
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281 YVRRALHRHYGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDTTEAMLKQG 340
                                         243 YVRAKLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 301
                                                                                231 YVELINQAARLNGYVDAGDSWRSMYETPSLE-----QDLERLFQELQPLYLNLHA 280
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                                                                                                                                                                                                                                                                                                                                                                    15 TAAQS----TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNM 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                             Match 31.3%; Score 1344; DB 4; Length 732; Local Similarity 41.8%; Pred. No. 4.8e-120; as 259; Conservative 119; Mismatches 204; Indels 3
                                                                                                                                                                                                     MSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEE 182
                                                                                                                                                                                                                                               NHT-----LKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLD 172
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One Post Office Square
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                                                                     US-08-989-299-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
 Matches
                 Best
                                   Query Match
                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Acton, Susan L. APPLICANT: Robinson, Keith
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                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS 420
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                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH 540
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1306 amino acids
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                             MOLECULE TYPE:
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COMPUTER: IF
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ZIP: 02109-2170
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                                                                                                                                                                                                                                                                                                     NAME: Arnold E., Beth REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/989,299 FILING DATE: 11-DEC-1997
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                                                                                                             TOPOLOGY:
                                                                                                                             STRANDEDNESS:
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               Local Similarity
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 255;
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Conservative 118; Mismatches 204;
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                   31.2%; Score 1337; DB 4;
41.7%; Pred. No. 5.9e-119;
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                                                                      SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/989,299 FILING DATE: 11-DEC-1997
                   ATTORNEY/AGENT INFORMATION: NAME: Arnold E., Beth
                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
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APPLICANT: Robinson, Keith E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1163 AGQRLATAMKLGFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTENELHGEKLGWP 1222
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                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.30
    REGISTRATION NUMBER:
                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                               CLASSIFICATION:
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                                                 GENERAL INFORMATION:
APPLICANT: Acton, Susan L.
APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES TH
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                  Sequence 8, Application US/08989299 Patent No. 6194556
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
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                                                                                                                                                                                                                                                                                                                                     596 MKLGYSKPWPEAMKLITGQPNMSASAMMNYFKPLTEWLVTENRRHGETLGWPEYNWAP 653
                                                                                                                                                                                                                                                                                                                                                                         558 LRIGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417 HIQYFMQYKDLPVTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN 475
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LENGTH: 732 amino acids
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TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 AQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 TDEAKADREVEEYDRTAQVLLNEYAEANWQYNTNITIEGSKILLEKSTEVSNHTLKYGTR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 TIEEQAKTFLLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDPASLFHYSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLMKMALDKIAFIPFSYLIDQWRWRYFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGD 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255;
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                                                                                       AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
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NAME: AINOID E., Beth
REGISTRATION NUMBER: 35,4
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin ReleCURRENT APPLICATION DATA:
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LENGTH: 1312 amino acids
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ZIP: 021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        649 TDEAKADREVEEYDRTAQVLLNEYAEANWQYNTNITIEGSKILLEKSTEVSNHTLKYGTR 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        709 AKTEDVSNEQNSSIKRIIKKLONLDRAVLPPKELEEYNQILLDMETTYSLSNICYTNG-- 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                       767 TCMPLEPDLTNMMATSRKYEELLWAWKSWRDKVGRAILPFFPKYVEFSNKIAKLNGYTDA 826
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                                                                                                                                                                                                                                                                                                                                                                                     20 TIEEQAKTELDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTL 79
                                                              1116 FDPGSKFHVPANVPYVRYFVSFIIQFQFHEALCRAAGHTGPLHKCDIYQSKEAGKLLADA 1175
                                                                                                                           1056 FLMKMALDKIAFIÞFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPÞVÞRSQGD 1115
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                                                                                                                                                                                                                                                                                                                                                       259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318
                                                                                                                                                                                                                                                                                                                                                                                                                       200 GDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPS-YISP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 AQMYPLQEIQNLTVKLQLQALQONGSSYLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQ 139
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::|| |:|| |:: : | ||: ::|||:|| ||: :|: :|| 1133
                                                                                                                                                                                                                                                                                          319 GLPNMTQGEWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG 377
                                                                                                                                                                                           378 HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 437
                                                                                                                                                                                                                                                          937 GLLPVPPEEWNKSMLEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHEMG 996
                                                                                                                                                           438 FLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETY 497
                            558 LRIGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSEVGW-STDWSP 612
                                                                                           498 CDPASLFHVSNDYSEIRYYTRTLYOFOFOEALCOAAKHEGPLHKCDISNSTEAGOKLFNM 557
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milarity 42.6%; Pred. No. 1.2e-118;
Conservative 112; Mismatches 213; Indels 18
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Acton, Susan L. APPLICANT: Robinson, Keith E.
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ADDRESSEE: FOLEY, HOAG & ELIOT LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                      650 TDEAKANREVEEYDRTAKVLWNEYAEANWHYNTNITIEGSKILLOKNKEVSNHTLKYGTW 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                      710 AKTEDVSNEQNSTIKRIIKKVQNVDRAVLPPNELEEYNQILLDMETTYSVANVCYTNG-- 767
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                                                                                                                                                                                                                                                        768 TCLSLEPDLTNIMATSRKYBELLMVWKSWRDKVGRAILPEFPKYVDFSNKIAKLNGYSDA 827
                                                                                                                                                                                                                                                                                      140 ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKOLRPLYEEYVVLKNEMARANHYEDY 199
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                                                                                                                             878 DGPTPAHLLGNMWAQTWSNIYDLVAPEPSAPSIDATEAMIKQGWTPRRIFKEADNFFTSL 937
                                                                                                                                                           259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGOKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318
                                                                                                                                                                                         828 GDSWRSSYESDDLE------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL 877
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                                                                                                                                                                                                                                                                                                                                                    80 AQMYPLQEIQNLTVKLQLQALQQNGSSYLSEDKSKRLNTILNIMSTIYSTGKVCNPDNPQ 139
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                              378 HIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEIN 437
                                                               938 GLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTSVNMEELVIAHHEMG 997
                                                                                           319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG 377
30.5%; Score 1310; DB 4; Length 1313; al Similarity 42.0%; Pred. No. 2.3e-116; 251; Conservative 115; Mismatches 214; Indels 18;
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                  167 SWRSEVGKQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDV 226
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                                                                    136 NLPLAKROQYNSLLSNMSQIYSTGKYCFPNKTASCWSLDPDLNNILASSRSYAMLLFAWE 195
                                                                                          107 VLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLMAWE 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08989299 Patent No. 6194556
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                                                                                                                                    81 TAENARRQEE----EALLSQEFAEAWGKKAKELYDPVWQNFTDPELRRIIGAVRTLGPA 135
                                                                                                                                                                   55 TEENVQNMNNAGDKWSAFLKEQSTLAQMYPLQEI----QNLT---VKLQLQALQQNGSS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 11-DEC-19
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                        21 LLLLLRPPPAALTLDPGLLPGDFAADEAGARLFASSYNSSAEQVLFRSTAASWAHDTNI 80
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                                                                                                                                                                                                                                       7 LLLSLVAVTAAQSTI-------EEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNI 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT
STREET: One Post Office Square
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APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES TI
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498 CDPASLEHVSNDYSEIRYYTRTLYQEQEQEALCQAAKHEGPLHKCDISNSTEAGQKLENM 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 FLLKQALTIVGTLPETYMLEKWRWMVFKGBIPKDQWMKKWWEMKREIVGVVEPVPHDETY 497
                                                                                                                                                                                                                                                                         h
Similarity 36.8%; Score 1283.5; DB 4; Length 1310;
75; Conservative 135; Mismatches 262; Indels 75; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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INFORMATION FOR SEQ ID NO:
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                             REFERENCE/DOCKET NUMBER: MITELECOMMUNICATION INFORMATION: 617-832-1000
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                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Acton, Susan L.
APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
 CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HO
                                                                                  NAME: Arnold E., Beth REGISTRATION NUMBER:
                                                                                                                                                 APPLICATION NUMBER: US/08/989, 299
FILING DATE: 11-DEC-1997
                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02109-2170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          633 YE--WND-----NEMYLFRSSVAYAMRQYFLKVKNOMILFGEEDVRVANLKPRISFNFF 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604 LDYFQFVTQWLQEQNERNGEVLGWPEYQWRPPLPNNYPEGIDLVTDEAEASRFVEEYDRS 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            585 LNYFEPLETWIKDONKNS--FVGW-STDWSPYADQSIKVRISLKSALG------DKA 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      405 GEIMSLSAATPKHLKSIGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVF 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 ASAWDEYNRKDERIKOCTOVTMDQLSTVHHEMGHVQYYLQYKDQPVSLRR-ANPGEHEAI 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 GQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCH 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 EHTFEEIKPLYEHLHAYVRAKLMNAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPF 285
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ICANT: Acton, Susan L.
ICANT: Robinson, Keith E.
ICANT: Robinson, Keith E.
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MOLECULE TYPE: protein US-08-989-299-6
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LENGTH: 737 amino acids
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US-08-989-299-11
                                                                                       Sequence 11, Application US/08989299

Sequence 11, Application US/08989299

Sequence 11, Application US/08989299

Sequence 11, Application US/08989299

SEQUENCE INFORMATION: AUGIOTENSIN CONVERTING ENZYME HOMOLOG APPLICANT: AUGIOTENSIN CONVERTING ENZYME HOMOLOG TIPLE OF INVENTION: AUGIOTENSIN CONVERTING ENZYME HOMOLOG THEREFOR TIPLE OF INVENTION: AUGIOTENSIN AUGIOTENSIN UNDER OF SEQUENCES: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 SAFLKEOSTLAOMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYST 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 RHYGAQHINLEGPIPAHLLGNMWAQTWSNIYDLVAPFPSASTMDATEAMIKQGWTPRRMF 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 KEAEKEFVSVGLPNNTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DERILMCTKVTMD 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                          532 CPPAPRSQGDEDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCKAAGHTGPLHTCDIYQS 591
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                                                                                                                                                                                                                                                                                                      652 WPQYTWTPNSARS 664
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                                                                                 CORRESPONDENCE ADDRESS:
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               STATE:
                                      CITY: Boston
                                                     STREET:
COUNTRY:
                                                                      ADDRESSEE:
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                                                       E: FOLEY, HOAG & ELIOT
One Post Office Square
       USA
                                                                             HOAG & ELIOT LLP
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MOLECULE TYPE: protein US-08-989-299-11
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Best Local Similarity
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MEDIUM TYPE: Floppy
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CURRENT APPLICATION DATA:
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TELEPHONE: 617-832-1000
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LENGTH: 615 amino acids
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 11 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 AKVKVCDYKDSTKCDLALDPEIEBVISKSRDHEELAYYWREFYDKAGTAVRSOFERYVEL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 STGKYCNPDNPQEC-LLLEPGLNEIMANSLDYNERLMAWESWRSEVGKQLRPLYEBYVVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                            187 KNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGOLIEDVEHTFEEIKPLYEHLHAYVRA 246
                                                                                                                                                                                                                                                                                                                                                                                                                188 NTKAAKLNNFTSGAEAWLDEYE-----DDTEEQQLEDI---FADIRPLYQQIHGYVRF 237
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                                                                                                                                                                                                                                                                                                                                                        238 RLRKHYGDAVVSETGPIPMHILGNWWAQQWSEIADIVSPFPEKPLVDVSAEMEKQAYTPL 297
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                                                                                                                                                                                                                                                                                               298 KMFQMGDDFFTSMNLTKLPQDFWDKSIIEKPTDGRDLVCHASAWDFYLIDDVRIKQCTRV 357
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                                                                                                                                                                                                                                                                 365 TMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLL 424
                                                                                                                                                                           1: |:| || || || : :!!| :|:|| || || :|:!! || 476
                                                                                                                                                                                                                                     358 TQDQLFTVHHELGHIQYFLQYQHQPFVYRTGANPGFHEAVGDVLSLSVSTPKHLEKIGLL 417
                                                                                                                                                                                                       425 SPDFOEDNETEINFILKQALTIVGTLPETYMLEKWRWMVFKGEIPKDOWMKKWWEMKREI 484
                                                        537 LDNCDIYGSARAGAAEHNMLSMGASKPWPDALEAFNGERIMSGKAIAEYFEPLRVWLEAE 596
                                                                                    539 LHKCDISNSTEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYEEPLFTWLKDQ 598
                                                                                                                  477 SGIEPEVVRSEKDFDAPAKYHISADVEYLRYLVSFIIQFQFYKSACIKAGQYDPDNVELP 536
                                                                                                                                              485 VGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALC-QAAKH-----EGP 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.4%; Score 1090; DB 4; Length 615;
25.4%; Score 1090; DB 4; Length 615;
21 Similarity 36.6%; Pred. No. 9e-96;
21 Similarity 36.6%; Pred. No. 9e-96;
224; Conservative 122; Mismatches 244; Indels 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02109-2170
                             599 N--KNSFVGWST 608
597 NIKNNVHIGWTT 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Release #1.0, Version #1.30
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US-08-989-299-12
                                                  RESULT 12
Sequence 12, Application US/08989299
Patent No. 6194556
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LENGTH: 694

TYPE: PRT
ORGANISM: Homo sapiens
                                                                 574 LL--ALKLGSSKPWPEVLKMLTGESEVSTNVFMTYFKPLLTWL 614
                                                                                            553 KLENMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWL 595
                                                                                                             514 SEEDFÖDGAKFHFSAGVPYÍRRYFLSLVLQFQFHETÍCKÁSGHMGPLHQCDIYNSKIÁGK 573
                                                                                                                                          494 DETYCDPASLEHVSNDYSFI-RYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQ 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 221; Conservative 104; Mismatches 228; Indels 30; Gaps
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Sequence 1, Application US/09440325A

Patent No. 6280994
                                                                                                                                                                      454 EVNELMHIALEKIAFIPEGYLMDLFRWKVEDGTIWKDIYNQEWWNLRRLKYQGLCDAIPH 513
                                                                                                                                                                                           435 EINFLLKOALTIVGTLPFTYMLEKWRWMVFKGEIPKDOWMKKWWEMKR-EIVGVVEPVPH 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                              399 EMCHFQYFLQYKNLSIIFRTGANPAFEEAVGSVITLSASSHKHLLNIGLLS--LLED--- 453
                                                                                                                                                                                                                                                 375 EMGHIQYDMAYAAQPELLRNGANEGFHEAVGEINSLSAATPKHLKSIGLLSDDFQEDNET 434
                                                                                                                                                                                                                                                                                  339 LGLALPPAPPSEWKKLMLMRPTDGREVECHISAWNFYQDDDFRIKKCAEVTTEDPLSTFH 398
                                                                                                                                                                                                                                                                                                             318 VG--LPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGK-GDFRILMCTKVTMDDFLTAHH 374
                                                                                                                                                                                                                                                                                                                                          279 GPIPAHLLGENTLAQSWVNILDPVLPFLKKIPEDVTKINKVQHWKPEKLMLEBAETFFTY 338
                                                                                                                                                                                                                                                                                                                                                                   260 GCLPAHLLGD-MWGREWTNLYSLTVPEGQKPNIDVTDAWVDQAWDAQRI-FKEAEKEFVS 317
                                                                                                                                                                                                                                                                                                                                                                                                229 ALWHSKYESDTLB-----QDLERLFQELRPLYLNPHTYVRRALHRHYGPELIDLR 278
                                                                                                                                                                                                                                                                                                                                                                                                                         201 DYWRGDYEVNGVDGYDYSRGOLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY-PSYISPI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 LSLESEL-EVMATSRDKEELLWAWQGWQDAVGRQICTTFEHYVELSNKAAQLNGVXKDMG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 LLLEPGINEIMANSLDYNERLWAWESWRSBYGKOLRPLYEEYYVLKNEMARANH-YEDYG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT ADPLICATION NUMBER: US/09/440,325A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 LFKVTQFKDPDVNGMLSKLQNIDKAALSKDELREYNELLAXLEMTYSNAQVCLNEGP--C 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Zacl: A FILE REFERENCE: 98-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sheppar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 MYPLOEIQNLTVKLOLQALQONGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPOEC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 ETETKIFLQFYDQTGEVVLNKFMEATWNYVTNITRKNQEEMMKDMER-SQFMIYFGTQAH 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 EEQAKTFLDKENHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTLAQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 23.1%; Score 990; DB 4; Length 694; Local Similarity 37.9%; Pred. No. 4.5e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastSEQ for Windows Version 3.0
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15.0%; Score 642.5; DB 4; Length 907;

Matches 172; Conservative 136; Mismatches 289; Indels 41; Gaps
571 TNPHYLYSOKLYPSEHLDIKDSVIINKLYKESLESFTKLPETIAADNWRYELFDGTYPKN 630
                                                  413 ATPKHLKSIGLLSPDFQEDNETE-INFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKD 471
                                                                                                       511 PNDFRVKACAQLGEPDFEQAHSLLVQTYYQYLYKDQSLLFREQASPVITDAIANAFAHLS 570
                                                                                                                                                         353 KGDERILMCTKVTMDDELTAHHEMGHIQYDMAYAAQPFLLRNGANEGEHEAVGEIMSLSA 412
                                                                                                                                                                                                           452 SAENTQNYTTKKMEVTAYRYEKSAGEPHLPKSYWTSSIFARVWS-KDMICHPAAALDMRA 510
                                                                                                                                                                                                                                        299 D----QAWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHP-TAWDL-G 352
                                                                                                                                                                                                                                                                                                                  394 HÁYMRRQLAGIYSNÞVGLSKDGÞÍÞÁHLÞGSLDGGDWSAHYEQTKÞFEEES--ETÞEÁML 451
                                                                                                                                                                                                                                                                                                                                                                    241 HAYVRAKLMNAY--PSYISDIGCLPAHLLGDMWGREWTNLYSLTVPEGQKPNIDVTDAMV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 617-832-100
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                         337 NIITISNEGAKLNGFANGGAMWRSAFDMSSKVHKAEF---DLNKQIDKIYSTIQFFYQLL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 EYVVLKNEMARANHYEDYGDYWRGDYEVNG-VDGYDYSRGQLIEDVEHTFEEIKPLYEHL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 ALNRDSKOSTICDKÖVÞÞÞCALQKIDMDSIFRNEKDASRLQHLWVSYVTATAKS-KÞSYN 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 TMSTIYSTGKVCNPDNPQECLLLEDGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 LDEAENVLTMEVRSTSMOAKOFDMASVTDEKVMROLGYVSFEGMSALAPSRFADYSQAQA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 SSNYWKTDNLQAPGSIKD--EEKLRSWLAGYEAEAIKVLREVALSGWRYFNDASPSLKLA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 907 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30
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FILING DATE: 11-DEC
CLASSIFICATION: 514
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Acton, Susan L.
APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADUL.
STREET: U.
STREET: U.
AA
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SOFTWARE: Patenti
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SYSTEM: PC-DOS/MS-DOS
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N: 514
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US-08-645-193B-15
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                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                      Matches 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/08645193B Patent No. 5962253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: not relevant MOLECULE TYPE: protein
                                    409 NDVKNLEK-NNTVSKINA---
                                                        111 DKSKRLNTILNTMSTIYSTGKYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRS 170
                                                                                             384 SNNI----YLLAIQNNSHIEITE 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                      324 ISEAAYILWILSPNHFGTKTIRNYHEFFMDKYGFEQLVNLKQILSDINGFGYPKKDSYSF 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin ReleCURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                51 NTNITEENVQNMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQONGSSVLSE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gotz, Friedrich
APPLICANT: Kempter, Christoph
APPLICANT: Jung, Gunther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kupke, Thomas
APPLICANT: Gotz, Friedri
                                                                                                                                                                                                                                                / Match
2.9%; Score 124; DB 2; Length 990;
Local Similarity 18.2%; Pred. No. 0.013;
Pes 153; Conservative 121; Mismatches 257; Indels 310; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                           1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHE-----AEDL--FYQSSLASWNY 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Esmond, Robert W. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   740 PLLEYYEPLINWLRNTNEIDQVVVGWDGEGTPFTVEEI 777
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      583 PILNYFEPLFTWLKDQNK--NSFVGWSTDWSPYADQSI 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    686 LKALCORELFWLSEG----CILSEDTT--EKLRETMKLGSSITWLKALEMISGKGELDAQ 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              631 KLNDRWWEIRNKYEGVRSPQPYNTSNLD--ALIHNSVSQVHS---PATRTLISYVLKFQI 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472 QWMKKWWEMKREIVGVVEPVPHDETYCDPASLFH--VSNDYSEIRYYTRTL----YQFQF 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                 990 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sterne,
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                    -----PVSTEI-----YSEIYF----- 437
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US-08-392-625-20
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/08392625 Patent No. 5837485
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                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue
                                                               APPLICANT: Kupke, Thomas
APPLICANT: Jung, G nther
APPLICANT: Kellner, Roland
TITLE OF INVENTION: Biosynthetic Process For The Preparation
TITLE OF INVENTION: Of Chemical Compounds
                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       692 SDIIP-----RIEVEKAIRMSRSRINDAF---RLNDNSLEFLGIQ 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              887 LYRSND-----TREY------KNLLAKL-----TNPKND 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  632 AYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVRVANLKPRISFNFFVTAPKNV 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          572 NVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPYADQSIKVRISLKSALGDK 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       856 FIVA---ISIDFLLDYLE---------------------------INKSEKEEILINNA--ED 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                799 DYCLLNSELYDYSIVDYVPEVYRYGGPHVIEDIENFFMYDSLL--SINIIQSE-FKIPKE 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   517 ----TRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLGKSEPWTLALE 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          763 KFFYIKFKED---EDFIK--LRLLRE------DEDY------SQIYSFIKNWK 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458 KWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYY- 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   708 KEQSEIIPKNRNKHENNLKDWESIHLSIPKTYQD----NEIQDYLLPEITELKVNNEIN 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 --LSAATPK------HLK---SIGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLE 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              648 IIAFGDNRLLLNLKNDKHLIILKKELKKHGRIRILESFINESNNERMLEIVTPLYKKTSL 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         592 TEEGIDSLPFCPRIIYKNIILKPATWKINSEMFSE---TENWLNRFATI-REKWHIPKDV 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 N------VQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGHIQYDM 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 IDVTDAMVDQAWDAQRIFKE---AEKFFVSVGLPNNTQG-----FWENSMLTDPG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485 ------HYNNYMNENDLETSQLNEAPLNSRNVNILNN--NRIYNTCLNLNLP---KSD 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 EEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGOKPN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438 --GNSIKG-YEDFAVISPILGSFNAGATFGRF-TGNFNIK-----KKNQLQKEIVH-- 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 EVGKOLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTF 230
                                                                                                                                            Wieland, Bernarke, Thomas
                                                                                                                                                                                                             Augustin, Johannes
Engelke, Germar
Rosenstein, Ralf
Kaletta, Cortina
                                                                                                                                                                                                                                                                                        Entian, Karl-Dieter
G tz, Friedrich
Schnell, No. 5837485bert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 20:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 990 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 ISEAAYILWILISPHEFGTKTIRNYHEFFMDKYGFEQLVNLKQILISDINGFGYPKKDSYSF 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 NDVKNLEK-NNTVSKINA------ 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 DKSKRLNTILNTMSTIYSTGKYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 SNNI----YLLAIQNNSHIEITE 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Esmond, Robert REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                             532 IDINDIFIGATENKLYLYSEKHDSRIVFVSNSMENYEFGSELYKELREISFEKTKFIQPI 591
                                                                                                                                                                                                                                                                                                                                                   291 IDVTDAMVDQAWDAQRIFKE---AEKFFVSVGLPNMTQG-----FWENSMLTDPG 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                231 EEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 EVGKQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 NTNITEENVQNMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSE 110
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                                                                                                                                                                                           355 DERILMCTKVTMDDFLTAHH-----EMGHIQYDMAYAAQPFLLRNGANEGFHEAVG 405
                                                                                                                                                                                                                                  592 TEEGIDSLPFCPRIIYKNIILKPATWKINSEMFSETENWLNRFATIRKWHIPKDVIIAFG 651
                                                                                                                                                                                                                                                                          338 N------VQKAVCHPTAWDLGK-----
                                                                          695 EIVTPLYKKTSLKEQSFIIPKNRNKHFNNLKDWFSIHLSIPKTYQD-----NFIQDYLLP 749
                                                                                                                406 EIMS-----LSAATPK-----HLK---SIGLLSPDFQEDNETEINFLLKQALT 445
                                                                                                                                                       652 DNRLLL-----NLLNDKHLIILKKELKKHGRIR-----ILESFINESNNERML 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
750 FITELKVNNFINKFFYIKFKED---EDFIK--LRLLRE---
                                     446 IVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFH 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSSSSWILLSLVAVTAAQSTIEEQAKTFLDKFNHE-----AEDL--FYQSSLASWNY 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --GNSIKG-YEDFAVISPILGSFNAGATFGRP-TGNFNIK-----KKNQLQKEIVH-- 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    560 LGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPYADQSIK 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    787 -SQIYSFIKNWKDYCLLNSELYDYSIVDYVPEVYRYGGPHVIEDIENFF-MYDSLLDSIN 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     506 VSNDYSFIRYY-----TRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLR 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   877 EEILINNA--EDLYRSND-----IREY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   620 VRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVRVANLKPRI 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Keliner, Roland
TITLE OF INVENTION: Biosynthetic process for the Preparation
TITLE OF INVENTION: Chemical Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 680 SENFEVTAPKNVSDIIP----- 716
                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,961A
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                  FILING DATE: 31-OCT-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                          PRIOR APPLICATION DATA:
TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                      APPLICATION NUMBER: US 07/876,791 FILING DATE: 30-APR-1992
                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 22-FE
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                    NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
                                                                                                                      APPLICATION NUMBER:
                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20, Application US/08466961A
o. 5843709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaletta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tz, Friedrich
                                                                                                          UMBER: US 07/784,234
31-OCT-1991
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958 CN----RIFGINP 966
                              717 LNDNSLEFLGIQP 729
                                            904 -----TNPKNDYEILKKEFPNLHEFLFNKISILENLKKTLQKSLYTSRSRIIGSFIHMR 957
                                                                                                         877 EEILINNA--EDLYRSND------IREY------KNLLAKL 903
                                                                          680 SFNFFVTAPKNVSDIIP-----RTEVEKAIRMSRSRINDAF---R 716
                                                                                                                                         620 VRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNOMILFGEEDVRVANLKPRI 679
                                                                                                                                                                           845 IIQSE-FKIPKEFIVA---ISIDELLDYLE-------INKSEK 876
                                                                                                                                                                                                       560 LGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPYADQSIK 619
                                                                                                                                                                                                                                         787 -SQIYSFIKNWKDYCLLNSELYDYSIVDYVPEVYRYGGPHVIEDIENFF-MYDSLLDSIN 844
                                                                                                                                                                                                                                                                         506 VSNDYSFIRYY-----TRTLYQFQFQEALCQAAKHEGFLHKGDISNSTEAGQKLFNMLR 559
                                                                                                                                                                                                                                                                                                        750 FITELKVNNETNKFFYIKFKED---EDEIK--LRLLRE------DEDY------ 786
                                                                                                                                                                                                                                                                                                                                        446 IVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYCDPASLFH 505
                                                                                                                                                                                                                                                                                                                                                                          695 EIVTPLYKKTSLKEQSFIIPKNRNKHENNLKDWESIHLSIPKTYQD-----NFIQDYLLP 749
                                                                                                                                                                                                                                                                                                                                                                                                          406 EIMS-----LSAATPK------HLK---SIGLLSPDFQEDNETEINFLLKQALT 445
                                                                                                                                                                                                                                                                                                                                                                                                                                          652 DNRLLL-----NLLNDKHLIILKKELKKHGRIR-----ILESFINESNNERML 694
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 DERILMCTKVTMDDFLTAHH-----EMGHIQYDMAYAAQPFLLRNGANEGFHEAVG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          592 TEEGIDSLPECPRIIYKNIILKPATWKINSEMESETENWLNREATIRKWHIPKDVIIAFG 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          532 IDINDIFIGATFNKLYLYSEKHDSRIVFVSNSMFNYEFGSELYKFLREISFEKTKFTQPI 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 IDVTDAMVDQAWDAQRIFKE---AEKFFVSVGLPNMTQG----FWENSMLTDPG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         485 -----HYNNYMNENDLEISQLNEAPLNSRNVNILNN--NRIYNTCLNLNLP----KSD 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 EEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGOKPN 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         438 --GNSIKG-YEDFAVISPILGSFNAGATFGRP-TGNFNIK-----KKNOLOKEIVH-- 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 EVGKQLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 NDVKNLEK-NNTVSKINA------ 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 DKSKRLNTILNTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 SNNI-----AFLKEK-----AFLKEK-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 ISEANYILWLLSPHEFGTKTIRNYHEFFMDKYGFEQLVNLKQLLSDINGFGYPKKDSYSF 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 NTNITEENVONMNNAGDKWSAFLKEQSTLAOMYPLQEIQNLTVKLOLOALQONGSSVLSE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHE-----AEDL--FYQSSLASWNY 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 142; Conservative 110; Mismatches 268; Indels 269; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 683 amino acids
322 NMTQGFWENSMLTDPGNVQKAVCH----PTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378
                               273 WEKRVDSTDRVYFVNHNTKTTQWEDPRTQGLQNEEPLPEGWEI-RYTREGVRYFVDHNTR 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46, Application US/08630916A
Patent No. 6011137
                                                               227 EHTFEEIKÞLYEHLHAYVRAKLMNAYPSYISÞIGCLÞAHLLGDMWGRFWTNLYSLTVÞFG 286
                                                                                                                                                             191 -----POPLPPGWERRVDDRRRVYYVDHNTRTTTWQRPTMESVRNFEQWQSQRNQL---- 241
                                                                                                                                                                                           168 WRSEVGKOLRPLYEEYVVLKNEMARANHYEDYGDYWRGDYE-VNGVDGYDYSRGOLIEDV 226
                                                                                                                                                                                                                           135 FEAAKSROPDGCMDPVRQQSG----NANTETLPSGWEQRKDPHGRTYYVDHNTRTTTWER 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                           127 YSTGKVCNPDNPQECLLLEPGLNEIMANS------LDYNERLWAWES 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           86 -----STTVEDPPVQEILTSSENNECIPSTSAELESEARSILEPDTSN------SRSSSA 134
                                                                                                                                                                                                                                                                                                                       72 FLKEQSTLAQMYPLQEI-----ONLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTNSTI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: PIYOZZI, U.T.,
APPLICANT: Kay, Brian K.
APPLICANT: FOWIKES, Dana M.
APPLICANT: FOWIKES, DANA M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                           44 LASEPADDTVNGESSSFAPTDN------ASVTGTPVVSEENALSPNCT----- 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                           12 VAVTAAOSTIEBOAKTFLDKFNHEAEDLFYOSSLASWNYNTNITEENVONMNNAGDKWSA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 03-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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US-08-844-059-2

RESULT 17

MOLECULE TYPE: protein

FILING DATE: 18-APR-1997 CLASSIFICATION: 536 CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: 9607999.1 APPLICATION NUMBER: 9607999.1 FILING DATE: 16-APR-1996 ATTORNEY/AGENT INFORMATION: ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 38.891 REGISTRATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPAN: 610-270-4478 TELEPAN: 610-270-5090 TELEX: FORDENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: LENGTH: 665 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear	PFKGE -: FRGI 	
RESULT 18 US-09-431-202-2 ; Sequence 2, Application US/09431202 ; Sequence 2, Application US/09431202 ; Sequence 3, Application US/09431202 ; Sequence 10: 6294175 ; Patent No. 6294175 ; CENERAL INFORMATION: No. 629417561 Compounds TITLE OF INVENTION: No. 629417561 Compounds OUNDERS OF SEQUENCES: 6 ; CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia COMPUTER: PA COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible	Dy 143 LLEPGLNE:MANSJJTENAMONDER: [1:1] 24 SKALDISYDKEIRTIDDYIEKVVA	059-2 2.6%; Score 113.5; atch 2.6%; Score 113.5; at Similarity 19.2%; Pred. No. 0 135; Conservative 99; Mismatche

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.6%; Score 113.5; DB 4; Length 665; Best Local Similarity 19.2%; Pred. No. 0.067; Matches 135; Conservative 99; Mismatches 231; Indels 239; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: 9314
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
592 AGDGEDRQILSGIA----KYY---PNEQELVGKKVQIVANLKPR----------
                                   636 -NDNEMYLFRSSVAYAMRQYFLKVKNQMILFGEEDVRVANLKPRISFNFFVTAPKNVSDI 694
                                                                             532 QMEGNKPAVEKEWNPDEVELKLNKDEIKFEDFDKVEIRVAEVKEVSKVEGSDKLLQFRLD 591
                                                                                                                     598 QNKNSFYGWSTDWSP-----YAD-QSIKVRIS----LKSALGDKAYEW--- 635
                                                                                                                                                             484 ------LTQIGLEE--VSSLENLSLADFPADVTVVAKGTPIFPRLNMEEEI-AYIKE 531
                                                                                                                                                                                                                                                472 IEP------ 483
                                                                                                                                                                                                                                                                                     488 VEPVPHDETYCDPASLFHYSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNS 547
                                                                                                                                                                                                                                                                                                                                                                        434 TEINFILKQALTIVGTL---PFTYMLEKWRWAVFKGEIPKDQW---MKKWWEMKREIVGV 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 665 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/844,059
                                                                                                                                                                                                     548 TEAGQKLFNMLRIGKSEFWTLALENV------VGAKNMNVRPLLNYFEPLFTWLKD 597
                                                                                                                                                                                                                                                                                                                                415 A-VDY--PRALEAVWTLISRTNKYIDETAPWVLDKDEALRDQLASVMSHWQASIRVVAHL 471
                                                                                                                                                                                                                                                                                                                                                                                                                361 LANDLGNLLNRTVSMINKYFDGQIPAYVEGVTEFDHVLAEVAE--KSIA----DFHTHME 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                        383 MAYAAQPFLLR-----NGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNE 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GWFVMKDGKMSKSKGNVVYPEMLVERYGLDPLRYYLMRNLPVGSDGTFTPEDYVGRINYE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 GFW---ENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGHIQYD 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 MV-----FVSVGLPN--MTQ 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LVEFFKAHPEFITPDGRLNEMLRNFIEPGLEDLAVSRTTFTWGVPVPSNPKHVVYVWIDA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 RAKLMNAYPSYISPIGCLPAHL-----LGDMWGRFWTNLYSLTVPFGQKPNIDV-TDA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 -SGWYSVS--DEEFFTESQLAEVFRDEAGNVTGGIAPSGHEVEWVSEESYFLRLSKYQDR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 WRGDYEVNGVDGYDYSRGQLIE--------DVEHTFEEIKPLYEHLHAYV 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 LLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYEDYGDY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 LLDISYDKFIRTTDDYHEKVVA-------QVFERLLAQDDIY--LGEY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 610-270-44'
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/431,202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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	213 DGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDMWG 272	Qу	
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	VGKQLRPLYE	Qy	
	: PDCSSSDG 62	дg	
	123MSTIYSTGKYCNP-DNPQECLLLEPGLNEIMANSLDY 158	Qy	
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	110 E 122	Qy	
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•	KIQ	Qy	
19	Query Match 2.4%; Score 104; DB 1; Length 834; Best Local Similarity 20.5%; Pred. No. 0.81; Matches 88; Conservative 59; Mismatches 142; Indels 140; Gaps	5 M C	
	ANTI-SENSE: NC 08-491-357-2	us-	
	MULECULE TYPE: protein HYPOTHETTCAL: NO		
	TOPOLOGY: not relevant	٠	
	ro over		
	LENGTH: 834 amino acids	٠. ٠	
	RMATION FOR SEQ		
	(215):	٠. ،	
	ATION		
	NAME: keed, Janet E. REGISTRATION NUMBER: 36,252	٠. ٠.	
	FORM		
	CLASSIFICATION: 435		
	CATION NUMBER		
	SUFTWAKE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:		
	SYSTEM: PC-DOS/MS-DOS	. ~.	
	MEDIUM TIPE: FIOPPY disk COMPUTER: IBM PC compatible		
	ABLE FORM:		
	ZIP: 19103-2307	•••	
	STATE: PA		
	CITY: Philadelphia	٠. ٠	
	Dann, Dorfman, He		
	CORRESPONDENCE ADDRESS:	٠	
9	TION: ALTERATIONS		
TCAI	OF INVENTION:	•••	
	Estojak, Joanne		
	Law, Susa		
	INFORMATION:		
	atent No		
	-08-491-357-2	. g	
	SULT 19	RE	
	629KMMKKYVSQGMILSAEHDGKLTLLTVDPAVPN 660	ρb	
	/ 695 IPRTEVEKAIRMSRSRINDAFRLNDNSLEFLGIQPTLGPPN 735	V	
	1	,	

110 B	Qy
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QNGSSVLS	Qy
Query Match 2.4%; Score 104; DB 3; Length 834; Best Local Similarity 20.5%; Pred. No. 0.81; Matches 88; Conservative 59; Mismatches 142; Indels 140; Gaps	Z & O
DEDNESS OGY: No. OGY: No. E TYPE: E TYPE: TICAL: NSE: NO.	US:
SEQUENCE CHARACTERISTICS: LENGTH: 834 amino acids TYPE: amino acid	
ION INFORMATION (215) 563-4100 (15) 563-4044	
п 🔪	
CLASSIFICATION: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/491,357 FILING DATE:	.,
ON DATA: BER: US/08/968,633	
OMPOTER REALIABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30	
USA 9103-2307	
ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720 CITY: Philadelphia CTATE: PA	
NVENTION: NVENTION: NVENTION: SEQUENCES:	
CANT: Golemis, Erica A. CANT: Law, Susan CANT: Estojak, JoAnne	
SULT 20 -08-968-633-2 Sequence 2, Application US/08968633 Pattent No. 6100384 GENERAL TURORMATION:	RESULT US-08- ; Sequ ; Pate
816 DLSRNAQLE 824	Дb
382 DMAYAAQPF 390	Qy
	gb
TQGFWENSMLTDPGNVQK	QV
273 REWTNLYSLTVPEGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLPNM 323 :	dd VQ
666LSQFQLLEQEITKPVENDISKWKPSQSLPTTNSGVSAQDRQLLCFYYD 713	Ф

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                                    714 QCETHFISL-----LNAIDALFSCVSSAOPPRIFVAHSKEVILSAHKLVFIG-DTL 763
                                                                                         273 REWINLYSLTVPFGQKPNIDVTDAMVDQAWDAQ--RIFKEAEKF------FVSVGLPNM 323
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                  382 DMAYAAQPF 390
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Search completed: March 13, 2003, 16:58:30 Job time: 29 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB seq
                                                                                                                                                                                                                                                                                                                                                  Score
     derived by analysis of the total score distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         March 13, 2003, 16:58:07; Search time 17 Seconds (without alignments) 2182.595 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                100
                                                                                                                                                                                                                                                                                                                                                  Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199416 seqs, 46092074 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-978-385-2
                                     Published_Applications_AA: *
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                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                    DB
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US-09-978-385-2
US-10-114-893-86
US-09-969-384-15
US-09-969-385-6
US-09-978-385-9
US-10-028-072-72
US-10-121-049-72
US-10-140-470-72
US-10-175-746-72
US-10-176-918-72
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US-10-142-431-72
US-10-142-431-72
US-10-142-431-72
US-10-142-431-72
US-10-142-431-72
US-10-142-431-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199416
                                Sequence 2, Appli
Sequence 13, Appl
Sequence 25, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 72, Appli
                                                                                                                                                                                                                                                                                                                                              Description
                Sequence
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376	376	376	376	376	376	376	376	376	376	376	376	376	376	376	376	376	376	376	376	376	376	376	990	1337	1359
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US-09-990-711-387	US-10-176-921-482	US-10-176-918-482	US-10-175-746-482	US-09-997-666-387	US-09-997-428-387	US-09-990-562-387	US-09-990-438-387	US-10-140-470-482	US-10-123-904-482	US-10-121-049-482	US-09-993-667-387	US-09-997-653-387	US-10-028-072-482	US-09-989-734-387	US-09-993-687-387	US-09-991-181-387	9 US-09-990-436-387	US-09-989-730-387	US-09-990-444-387	US-09-989-735-387	US-09-989-293A-387	US-09-992-598-387	US-09-846-996A-1	US-09-964-899-19	US-09-969-384-23
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ALIGNMENTS

US-09-978-385-2

Sequence 2, Application US/09978385 Patent No. US20020177211A1

GENERAL INFORMATION:
APPLICANT: Piddington, Christopher S.
APPLICANT: Pettie, Charles
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
FILE REFERENCE: 99-24C1

CURRENT APPLICATION NUMBER: US/09/978,385
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/133,952
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/151,181
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 09/563,516

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                                                                                                                                                                                                                                            ; LENGTH: 805
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-385-2
                                                                                                                                                                                 Query Match
Best Local S
Matches 805
                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
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                                                           NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL
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                                                                                                                                                                                            Similarity
                                                                                                                                                                                  Conservative
                                                                                                                                                                                               100.0%; Score 4291; 100.0%; Pred. No. 0;
                                                                                                                                                                                  0;
                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                ВB
                                                                                                                                                                                  0;
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                                                                                                                                                                                                             Length 805;
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Homo sapiens

DB

Length

805;

0

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GENERAL INFORMATION:
APPLICANT: McCoy, John M.
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Bowman, Michael R.
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Carin-Duckett, McKeough
                               APPLICANT: Kelleher, Kerry S.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
FIIRE OF INVENTION: SECRETED PROTEINS AND POI
FILE REFERENCE: GI 6000-10A
CURRENT APPLICATION NUMBER: US/10/114,893
CURRENT FILING DATE: 2002-04-02
EARLIER APPLICATION NUMBER: 09/413,232
EARLIER APPLICATION NUMBER: 09/413,232
EARLIER FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
SOFTWARE: Patentin Ver. 2.0
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US-10-114-893-86
    SEQ ID NO
LENGTH:
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           RESULT 3
US-09-969-384-13
IS-09-969-384-13
Sequence 13, Application US/0
Publication No. US20020192740
GENERAL INFORMATION:
APPLICANT MOORE, et al.
TITLE OF INVENTION: Human Go
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PRIOR APPLICATION NUMBER: PCT/US01/10542
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/236,384
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/194,118
PRIOR FILING DATE: 2000-04-03
NUMBER: OF SEQ ID NOS: 27
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SEQ ID NO 13
LENGTH: 711
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Best Local Similarity
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CURRENT FILING DATE: 2001-10-03
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LOCATION: (240)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (219)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                              SFVGWSTDWSPYADQSIKVRISLKSALGDKAYEWNDNEMYLFRSSVAYAMRQYFLKVKNQ
                                                                                                                                                                                                                                             REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/099 Publication No. US20020192749A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/969,384
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/US01/10542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/194,118
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/236,384
PRIOR FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: PT055P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Moore,
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (219)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (240)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   482 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK 541
                                                                                                                                                                                                                                                                                                                                                                                            182 EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH 241
                                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 MINIAGDKWSAFIKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 60
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                                                                                 GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK 481
                                            TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360
                                                                                                                                               TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 421
                                                                                                                                                                                                          WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC
                                                                                                                                                                                                                                                                                                               AYVRAKLMNAYPSYISDIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 301
                                                                                                                                                                                                                                                                                                                                                                      EYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLH
                                                                                                                                                                                                                                               WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 361
                                                                                                                                                                                                                                                                                          AYVRPKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYXLTVPFGQKPNIDVTDAMVDQX
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US-09-978-385-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Piddington, Christopher S. APPLICANT: Petrie, Charles
APPLICANT: Shoemaker, Kimberly E. APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: ZACEZ: A HUMAN METALLOENZYME FILE REFERENCE: 99-24C1
CURRENT APPLICATION NUMBER: US/09/978,385
CURRENT APPLICATION NUMBER: 2001-10-16
CURRENT FILING DATE: 2001-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/133,952
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/151,181
PRIOR ETILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 09/563,516
PRIOR FILING DATE: 2000-05-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mouse
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301 AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDDGNVQKAVCHPTAWDLGKGDFRILM 360
                                                      181 EEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKDLYEHL 240
                                                                                                                                                                                                       121 NTMSTIYSTGKVCNPKNPQECLLLEPGLDEIMATSTDYNSRLWAWEGWRAEVGKQLRPLY
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                                                                                                                                                                                                                                                                                                                                                                               1 MSSSSWLLLSLVAVTAAQSTIEEQAKTELDKFUHEAEDLFYQSSLASWNYNTNTTEENVQ 60
                                                                                                                            EEYVVLKNEMARANNYNDYGDYWRGDYEAEGADGYNYNRNQLIEDVERTFAEIKPLYEHL
                                                                                                                                                                                                                        NTMSTIYSTGKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLY 180
                                                                                                                                                                                                                                                                               KMSEAAAKWSAFYEEQSKTAQSFSLQEIQTPIIKRQLQALQQSGSSALSADKNKQLNTIL 120
                                                                                                                                                                                                                                                                                                                  NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTYKLQLQALQQNGSSVLSEDKSKRLNTIL 120
                                                                                                                                                                                                                                                                                                                                                         MSSSSWLLLSLVAVTTAQSLTEENAKTFLNNFNQEAEDLSYQSSLASWNYNTNITEENAQ 60
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APPLICANT: Piglington, Christopher S.
APPLICANT: Petrie, Charles
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
FILE REFERENCE: 99-24C1
CURRENT APPLICATION NUMBER: US/09/978,385
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/133,952
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/151,181
PRIOR APPLICATION NUMBER: 60/151,181
PRIOR APPLICATION NUMBER: 09/151,781
PRIOR APPLICATION NUMBER: 09/151,781
PRIOR APPLICATION NUMBER: 09/563,516
PRIOR APPLICATION NUMBER: 09/563,516
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 09/563,516
PRIOR FILING DATE: 2000-05-03
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US-09-978-385-9
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Best Local (
                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 9
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                                                                                                                                                                                                                                                                                           LENGTH: 805
TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version
61 KMSEAAAKWSAFYEEQSKTAQSFSLQEIQTPIIKRQLQALQQSGSSALSADKNKQLNTIL 120
                           61 NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120
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                                                                                                                 1 MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ
                                                                                   MSSSSWLLLSLVAVTTAQSLTEENAKTFLNNFNQEAEDLSYQSSLASWNYNTNITEENAQ 60
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                                                                                                                                                                              Conservative 60; Mismatches 86;
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INVENTION:
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                              Tumas,Daniel
Watanabe,Colin K
Wood,William
                                                                                           Smith, Victoria
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Gurney, Austin L.
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                                                                            Stewart, Timothy A.
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PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062285
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APPLICATION NUMBER: 60/073612
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APPLICATION NUMBER: 60/069212
FILING DATE: 1997-12-11
APPLICATION NUMBER: 60/069278
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OR FILING DATE: 1998-06-24
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OR APPLICATION NUMBER: 60/088730

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OR APPLICATION NUMBER: 60/088741

OR FILING DATE: 1998-06-10

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FILING DATE: 1998-06-18
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KREIVGVVEPVPHDETYCDPASLFHVSDDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
                  KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
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                                                                                       IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWWVFKGEIPKDQWMKKWWEM
                                                                                                                                      CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/088858
                                                                   IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM
                                                                                                                                                                                                            AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM
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US-10-121-049-72
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US-10-121-049-72
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CURRENT FILING DATE: 2002-04-12
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                                                                        AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM 360
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                                                          AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM
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Godowski, Paul J.
Gurney, Austin L.
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Pred. No. 1.9e-239;
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US-10-123-904-72
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 72
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
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Filvaroff, Ellen
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99.8%;
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    Mismatches

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SEQ ID NO 72
LENGTH: 555
TYPE: PRT
ORCANISM: Homo Sapien
US-10-140-470-72
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; Sequence 72, Application US/10140470

; Publication No. US20030022331A1
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APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: rilvaroff, Eller
APPLICANT: Gao, Wei-Qiang
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
CURRENT FILING DATE: 2002-05-06
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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61 NMNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTIL 120 	Db Db	
1 MSSSSWILLSLVAVTAAQSTIEBQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQ 60 	Qy	
Match 69.4%; Score 2979; DB 9; Length 555; Local Similarity 99.8%; Pred. No. 1.9e-239; Local Similarity 91.8%; Pred. No. 1.9e-239; Length 555; Local Similarity 91.8%; Pred. No. 1.9e-239; Length 555; Length 555; Length 555; Local Similarity 91.8%; Pred. No. 1.9e-239; Length 555; Length 555; Local Similarity 91.8%; Pred. No. 1.9e-239; Length 555; Length 555; Length 556;	Query Ma Best Loo Matches	
PR SM	ıs-:	
Application removed - See File Wrapper or Palm ROF SEQ ID NOS: 550 PRO 72 PRO 1550 P	Prior NUMBER SEQ ID	•
FERENCE: P3330R1C353 APPLICATION NUMBER: US/10/175,74 FILING DATE: 2002-06-19	CUR	
CANT: Zhang, Zemin OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC OF INVENTION: ACIDS ENCODING THE SAME	APP TIT	
APPLICANT: Watanabe, Colin K APPLICANT: Wood, William	APP	
CANT: Stewart, Timothy A. CANT: Tumas, Daniel		
CANT: Gurney,Austru L. CANT: Sherwood,Steven CANT: Smith,Victoria		
CANT: Goddwyski, Paul J.		
CANT: Filvaroff, Elen CANT: Filvaroff, Elen CANT: Gao Wai-Olang		
Baker, Kevin P.		
7.746-72 Ce 72, Application US/10175746 ation No. US20030027270A1 L TNFORMATION:	Seque Seque Publi	
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41 KCDISNSTEAGQKL 554	0у 5	
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81 KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH 540	Qy 4	
IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEM 48	Db 421	
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CTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKS	. ω	
AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM 360	Db 301	
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	Db 241	
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1 EEYYVLKNEMARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLLEDVEHTFEELKFLIEHL 240	Db 18	

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; TYPE: PRT; ORGANISM: Homo Sapien US-10-176-918-72
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                                                                                                     TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C382

CURRENT APPLICATION NUMBER: US/10/176,918

CURRENT FILING DATE: 2002-06-20

Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NO 72

LENGTH: 555
     Query Match
Best Local Similarity
Matches 553; Conserv
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APPLICANT: Baker, Ke
APPLICANT: Beresin
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Publication No.
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Godowski, Paul J.
Gurney, Austin L.
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99.8%;
  Score 2979; DB 9;
Pred. No. 1.9e-239;
1; Mismatches 0;
                               Length 555;
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            SEQ ID NO 72
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                                                        APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93330R1C288
CURRENT APPLICATION NUMBER: US/10/176,921
CURRENT FILING DATE: 2002-06-20
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maur
                           Prior Application removed - NUMBER OF SEQ ID NOS: 550
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LENGTH:
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Watanabe, Colin K
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Gurney, Austin L.
Sherwood, Steven
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E OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC OF INVENTION: ACIDS ENCODING THE SAME REFERENCE: P3330R1C154
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Godowski, Paul J.
Gurney, Austin L.
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                                                                Watanabe, Colin K
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Sequence 72, Application US/10140474
Publication No. US20030032156A1
GENERAL INFORMATION:
APPLICANT BAKET, Kevin P.
APPLICANT Beresini, Maureen
APPLICANT Desnoyers, Laura
APPLICANT Desnoyers, Luca
APPLICANT Desnoyers, Luca
APPLICANT Geo. Wei-Qiang
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APPLICANT Geowei-Qiang
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APPLICANT Guney, Austin L.
APPLICANT Sherwood, Steven
APPLICANT Smith, Victoria
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 72
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CURRENT FILING DATE: 2002-05-03
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ORGANISM: Homo
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            KCDISNSTEAGQKL 554
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                                                       KREIVGVVEPVPHDETYCDPASLFHVSDDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
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Pred. No. 1.9e-239;
1; Mismatches 0;
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RESULT 16
US-10-142-431-72
Sequence 72, Application US/10142431
Publication No. US20030036179A1
GENERAL INFORMATION:
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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
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LENGTH: 555
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/140,474
CURRENT FILING DATE: 2002-05-06
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APPLICANT:
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                                              Beresini, Maureen
DeForge, Laura
               Desnoyers, Luc
Filvaroff, Ellen
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LENGTH: 555
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CURRENT APPLICATION NUMBER: US/10/142,431
CURRENT FILING DATE: 2002-05-10
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KCDISNSTEAGQKL 554
                                                                     KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH 540
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                              KCDISNSTEAGQKL 554
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RESULT 17 US-10-143-114-72

Sequence 72, Appropriate Publication No.

Application US/10143114 No. US20030036180A1

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                                          KREIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLH
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KCDISNSTEAGQKL 554
                              KREIVGVVEPVPHDETYCDPASLFHVSDDYSFIRYYTRTLYQFQEQEALCQAAKHEGPLH
                                                                                         IGLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKNRWAVFKGEIPKDQWMKKWWEM
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Watanabe, Colin K
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Stewart, Timothy A.
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CURRENT FILING DATE: 2002-05-06
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C59
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Local Similarity 99.8%;
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    Mismatches

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Pred. No. 1.9e-239;
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US-10-142-419-72
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LENGTH: 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/142,419
CURRENT FILLING DATE: 2002-05-10
Prior Apploication removed - See File Wrapper
NUMBER OF SEQ ID NOS: 550
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                            AWDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILM 360
                                                                       HAYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFFGQKPNIDVTDANVDQ 300
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Godowski, Paul J.
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Pred. No. 1.9e-239;
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LENGTH: 261
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Best Local Similarity 99.6%;
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CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/US01/10542
PRIOR EILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/236,384
PRIOR APPLICATION NUMBER: 60/236,384
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
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TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PT055P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 27
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                                                                   181 AYVRPKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA
                                                                                      242 AYVRAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQA 301
241 WDAQRIFKEAEKF 253
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                                                                                                                                                                                                                                                                                          1 MNNAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILN 60
                                                                                                                                                                                                                   TMSTIYSTGKYCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYE 120
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-Q-ggn2_1/USPTO_Spool_V5809178385/runat_28022003_104716_1342/app_query.fasta_1.967
-Q-ggn2_1/USPTO_Spool_V5809178385/runat_28022003_104716_1342/app_query.fasta_1.967
-DB-GenEmb1 -QFMT=fastap -SUFFIX=pin.rge -MIMATCCH=0.1 -LOOPCLT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 - TRANS-human40.cdi - LIST=45
-DOCALIGN=200 -THR_SCORE-pot -THR_MAX=100 -THR_MIN-0 -ALIGN=20 -MODE-LOCAL
-DOCALIGN=200 -THR_SCORE-pot -THR_MIN-0 -MAXLEN-200000000
-USTEMT=pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USTEMT=98385_6CGN 1_1_3745_6runat_28022003_104716_1342 -NCPU-6 -ICPU-3
-USER-US09978385_6CGN 1_1_3745_6runat_28022003_104716_1342 -NCPU-6 -ICPU-3
-NSARN_TIMEOUT=30 -THREADS-1 -XGAPOP-10 -XGAPEXT=0.5 -FGAPOP-6 -FGAPEXT=7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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161 ArgLeuTrpalaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProl	### GlnmetTyrProLeuglnGluIleglnAsnLeuThrVallysLeuglnLeugln	1 MetSerSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaG:	gnment Scores: d. No.: re: cent Similarity: t Local Similarity ry Match:	ARI35178 EVENITION Sequence 3 from patent US 6194556. RRSION ARI35178 ARRI35178 ARRI35178.1 GI:14124083 EVENORDS UNKNOWN. UNGANISM Unknown. Unclassified. 1 (bases 1 to 2415) ACTON, S. Laurene. and Robison, K. Earl. ACTOREASI JOURNAL ARJOLERSIN CONVERTING enzyme homolog and therapeut diagnostic uses therfor Agiotensin converting enzyme homolog and therapeut Location/Qualifiers Source 1. 2415 SE COUNT 743 a 483 c 555 g 634 t
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                                                                                                  Angiotensin converting enzyme homolog and Patent: WO 0212471-A 3 14-FEB-2002; Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthería; Primates; Catarrhini; Hominidae; Homo.
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PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700
                         CAGATGATTCTTTTTGGGGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCC
                                         GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer 680
                                                                            TACCTGTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAAT
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Sugano, S. and Komatsu, T.
ACE-analogous gene
Patent: JP 2001046072-A 1 20-FEB-2001;
OTSUKA PHARMACEUT CO LTD
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A61K39/395, PC A61K39/395,
PC A61K39/395,A61K48/00,A61P9/12,C07K14/47,C07K16/08,C12N1/15,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 2418)

CE 1 (bases 1 to 2418)

RS Christopher, D.S. and Nicola, B.
MPROT15 polypeptide and MPROT15 polynucleotide

All Patent: JP 199318472-A 1 24-NOV-1999;

SMITHKIAINE BEECHAM CORP PUBLIC LTD CO

OS HOMO sapiens (human)

PN JP 199318472-A/1

PD 24-NOV-1999

PF 22-JAN-1999 JP 1999014949

PF 22-JAN-1999 GB 9810373:2;18-AUG-1998 GB 9818009:4 PI

CHRISTOPHER D SAZAN, NICOLA BAGESU

PC C12N15/09,A61K31/00,A61K31/00,A61K31/00,A61K31/00,A61K31/70,

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                          SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740
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 IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu
                                                                                  GAAAAGGCCATCAGGATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAAC
                                                                                                GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn
                                                                                                                                          TTTAATTTCTTTGTCACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTT
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TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln
                                     ATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC
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A61K37/64,
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FH Key
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patent: JP 2001046072-A 2 20-FEB-2001;
OTSUKA PHARMACEUT CO LTD
OS Unknown
DP 2001046072-A/2
PD 20-FEB-2001
PF 06-AUG-1999 JF 1999223892
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Sugano, S. and Komatsu, T.
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PI SUMIO SUGANO, TAKAMI KOMATSU
PC C12N15/09, A61K31/00, A61K31/7088, A61K38/00, A61K38/55,
A61K39/395, PC A61K39/395,
PC A61K39/395, A61K48/00, A61P9/12, C07K14/47, C07K16/08, C12N1/15, PC
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GINGINASNGIYSETSETVAILEUSETGII	GlnAsnGlySerSerValLeuSerGl
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	LeuThrValLy, LeuThrValLy,

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Submitted
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Donoghue, M., Woolf, B., Robison, K.
Direct Submission
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Donoghue,M., Hsieh,F., Baronas,E., Godbout,K., Gosselin,M., Stagliano,N., Donovan,M., Woolf,B., Robison,K., Jeyaseelan, Breitbart,R.E. and Acton,S.
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/protein_id="AAF99721.1"
/db_xref="GI:9802433"
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                                                                                                                               TyrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660
                                                                                                                                                                                                                                                                          AATTCTTTTGTGGGATGGAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTG
                                                                                                                                                                                                                                                                                     AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal 620
                                                                                                                                                                                                                                                                                                                        GTAAGGCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAAGACCAGAACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAATGTGACATCTCAAACTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis
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SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740
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                                                                                 TTTAATTTCTTTGTCACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTT
                                                                                           PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700
                                                                                                                                                                                                                                         ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640
                                                                                                                                                                                                                            AGGATAAGCCTAAAATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATG
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MetSerSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr

(1-3334)

Gaps:

ATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACC

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REFERENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 3334)
Piddington, C.S., Petrle, C.R., Shoemaker, K.E. and Bishop, P.
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Patent: WO 0070032-A 1 23-NOV-2000;
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IWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARSGENPYASIDISKGENNPGFQNT
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400	TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe	381	Qy
1174	TGCACAAAGGTGACAATGGACGACTTCCTGACAGCTCATGAGATGGGGGCATATCCAG	1115	Db
380	ysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGl	6	Qy
360 1114	LysalawalCysHlsProThraLaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet	J +	B 4
0		995	Db
4	roAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln	321	Qy
320 994	AlaTrpAspAlaGlnargIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 	301 935	pb dy
w	TGACAGTTCCCTTTGGACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAG	875	문
300	euThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln	œ	Qy
280 874	CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer 	261 815	ДУ
ست	CATGCCTATGTGAGGCCAAAGTTGATGAATGCCTATCCTTATATCAGTCCAATTGGA	755	Db
260	isAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleG1	241	Qy
240 754	GlnLeulleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu		Дb
	ATTATTGGAGAGGAGA	w	ДЬ
220	rTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGl	0	Qy
200	GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly	181 575	ο Оу
7		515	Дb
œ	xgLeuT xpA laT xpG luSe x T $xpAxg$ Se x GluValGl y L y SGlnLeuA x g x P x OL	161	Qу
160 514	Cyburgureureureureureureureureureureureureureu	(FI a	B 2
١ U	CARTERITERITERITERITERITERITERITERITERITER	Δ.	Q ·
л 4-	AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 	121 395	Db Oy
120 394	Oliver in Substy Set vertice user of the Sprysser Lysargheuaspith file Leu	335	B 4
ú	CAAATGTATCCACTACAAGAAATTCAGAAATCTCACAGGTCAAGCTTCAGCTGCAGGGT	275	g B
100	GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu	00	Qy
274		215	Db
	AsnMetAsnAsnAlaGlvAsnIvsTrnserAlaDhelenivsClnGlnserThrionA	σ	QΨ
60	l TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 	41 155	Db 04
154	ATTGAGGAACAGGCC	95	Db
40	LysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPh		Qy

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                                                             TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnTleThrGluGluAsnValGln
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                         AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu
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                                               AATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAA
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NLYSLTVPFGQKPNLDYTDAMYDQAWDAQRIFKEAEKFFYSVGLPNMTAGAPFFLL
RNGANEGFHEAVGEINSISAATPKHLKSIGLLSPDFQEDNETELMGHLIQALTYGFLL
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DYSFIRYTTRTLYGFQPGABALQAAKHEGPLHKCDISNSTEGAGGXLFNMLRLGKSSPW
TLALEMVYGAKMNWARPLLNYEEPLFTWIKKDQNKNSFVGWSTDWSPYADQSIVVRISL
KSALGDKAYEWNDNEMYLFRSSVAYAMAQYFLKVKNQMLLFGEEDVFVANIK PRISFN
FFYTAPKNVSSIIPRTEVEKAIRWSRSRINDAFRLNDMSLEFIGIQPTQAPPQPPS
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/db_xref="GI:21523782"
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/db_xref="taxon:9606"
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                                                                              LysargGluTleValGlyValValGluProValProHisAspGluThrTyrCysAspPro
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                                                               AAGCGAGAGATAGTTGGGGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCC
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       Homo sapiens
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Sequence 1 :
AX431513
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         Eutheria;
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        Chordata;
Primates;
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LASWNYKNNITEENVQNNNNAGDKWSAFIKEQSTLAQWYPLQEIQNLTYWKLQLQALQQ
NGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNEDNPQECLLLEPGLNEIMANSLDYNE
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RGQLIEUVEHTFEEIKPLYELYEELYALTYNAAVAAQFFYT
NLYSLTYVEFGQKPNIDYTDAMYDQAWDAQRIFKEAEKFFYSVGLPNMTQGFWENSMLT
DPGNVQKAVCHPTAWDLGKGDFRILMCTKTWNDDFTJAHEMGHIQYDWAYAAQFFLL
RNGANEGFHEAVGFIKSISAATPKHLKSIGLLSPDFDEDNETEINFLKQALTYUGTTL
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PETYMLEKWRMWYEKGEIPKDQWMKKWWEMKREIVGVVEPVHDETYCDPASLFHVSN
DYSFIRYTTTLYQFQRQEALCQAAKHGGPLHKCDISNSTEAGQKLFNNLRCAGSEPW
TLALENVYGAKMNWYEPLLNYEEPLFTWIKLDOMKUSFYGWSTDWSPYADOSIKYRISIN
KSALGDKAYEWNUNDHLIFRSSVAYAMRQYFLKVKNQMILFGEEDVRVANLKPRISIN
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                                                                                          TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480
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CATGAAGCTGTTGGGGAAATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAAATCC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3405)
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Submitted (02-MAR-2000) School of Biochemistry and Molecular Biology, University of Leeds, Mount Preston Street, Leeds, West Yorkshire LSS 9JT, UK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   functional expression as a captopril-insensitive carboxypeptidase
J. Biol. Chem. 275 (43), 33238-33243 (2000)
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RGOLIEDVEHTEEIK PLYEHLHAYVRAKLMAAYESY ISPIGCLEPAHLLGDWMGRFWF
NLYSLTVPEGOK PNID VTDAMVDQAMDAQRIFK EARKFFVSVGLENMTOGFWENSMLT
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1046 a

US-09-978-385-2 (1-805) x AF241254 (1-3405) Percent Similarity: Best Local Similarity: Alignment Scores: 4291.00 100.00% 100.00% 100.00% Length:
Matches:
Conservative: Mismatches: Indels: 3405 805 0 0 0

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ATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC 223

TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60

TATCAAAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAA 80

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eValGly	OASI CGAT	EMet	aG1r ACA	Sp/ ACC	CACAC	PTCTG	 ATATI PheTr	GACAC TqIle	yGlnI	euLeuGly	AAAC	laLys	/alGluHi	BACTATGA	GAAAA	uLys	GluSerT	CCAGGTT	ProGly	IleTyrs	TCAGTGCT	erVa	CAAGAAA
ThrLeup	PheGlnGluA	3-5	ProPhe CCTTTT	PheLeuThr	Trp		illill AGGAG	CCA	ProAsn	AspMet GATATG	HIIII ATGAA	t As	sThrPhe		GAG	GluMe	rpargse:	GAATO	uAsno	erThrG1	TCTCAGAA	uSerc	TTCAGAA
roPheThr CATTTACT	SPASNO ACAATO	erAla CTGCAG	ELeuLeuAr CTGCTAAG	Alar GCTC	GlyI GGG	CAT	CGA	AGAT	IleAs	TrpGly# TGGGGT#	TGCCTATCC	GAAGAG <i>i</i> AlaTyri	GluGluj	GGGGTAG	GCAAGA	AlaAr	rGluValG	AAATAATG	P A	llyLysVal	GACAAG	AspLys	TCTCACA
TYTME	luThrGlu AAACAGAA	laThrPro	gAsnGl) AAATGG <i>F</i>	lisHisGlu ATCATGAC	sGly/ 	AACGGA		TACTG!	lThrAs	rgPheTz GATTTTG	CTTCCTA	TAAAC oSerT	[leLysPr	ATGGCTAT	Ğ.—	laAsnH	lyLysg 		تست دلا	lCysAsnPro	 AGCAAAC	Ø	GTCAAGC
etLeuGluL GTTAGAGA	IleAsr ATAAAC	LyshisL AAGCATT	aAsı -	BluMetGlyI BAGATGGGGG	eArg CAGG	CCCAGGA	TATO	TGCAATC	pAlaMe	PThrasn GACAAAT	TATCAGT	ATTA	OLeu	TRASPTYR	TATGA	Tyrcl	InLeuAr	GTTTAGAC	AGAT	roAspAsn		rgLeuAs	TTCAGCT
ysTrpAr AGTGGAG	PheLeuLe	euLysse TAAAATC	nGluGlyPhe GAAGGATTC	HisIleG CATATCC	[IleLeuMe ATCCTTAT	AAATGTTC	TGGTC	TITITITE GENERAL CO	ValAsp	LeuTyrs	CCAATTG	CAT	[yrGluHis]	rSerArgG AGCCGCG		AspTy	gProLeu CCamma	TACAAT	CCACAA	ProGln	CAATI	hrile	GCAGGC
g 460 G 1483	u 440 1423	er 420 C 1363	ne 400	11 380 11 AG 124:	et 360 TG 118:	III 340 AG 112:	1 1 1 3 2 3 2 3 2 3 2 3 2 3 2 3 2 3 2 3	G 10	1n 30	er 280	Zoo	TT 82		31y 220 111 3GC 763	 GG 7	14	uTyr 18	111 GAG 583	AA 52	- L	CTA 4	Leu 1	TCTT 40

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503	TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 8	781 2444	Ωу
80	IlePheThrGlyIleArgAspArgLysLysAsnLysAlaArgSerGlyGluAsnPro 7	യ് ത്	Дb
760	TleTrpLeu1leValPheGlyValValMetGlyValIleValValGlyIleValIleLeu	2 4	Db 42
740 2323	erLeuGluPheLeuGly: 		, pp 64
720 2263	uLysalaIl AAAGGCCATO	8 8	Db dy
700 2203	PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal	ο - ο	DB 25
680 2143	GliMetileLeupheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer	0 0	DB QY
660 2083	TYFLGUPRAKIGSERSETVALALATYRALAMETARGINTYRPHELGULYSVALLYSASN) Db
640 2023	ArgileSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet	0 0	B 5
620 1963	AsnSerPheValGlyTrpSe	00	, pp qq
600 1903	ValArgProLeuLeu	184	2 dd 19
580 1843	GlyLysSerGlu	178) B Q
560 1783	LysCysAspI AAATGTGACA	17	da da
540 1723		<u>1</u> 1	B 2
520 1663	1 AlaSerLeuPheHis 	16 5	d da
500 1603	31 LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 	y 48 b 154	Db Qy
1543	61 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 	14 4	Qy

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                             1 MetSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
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Submitted (25-JUL-2000) Takami Komatsu, the Institute of Medical Science, Virology; 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:komatsu@ims.u-tokyo.ac.jp, Tel:81-3-5449-5283(ex.75283),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning, expression analysis and chromosomal localization of novel ACE like enzyme
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DPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGHIQYDMAYAAQPFLL
RNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDMETFEINFLLKGALTIVGTL
PETYMLEKWRMVFKGEIPKDOWMKKWWEMKREIVGVVEPVPHDETYCDPASLFHVSN
DYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLGKSEPW
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Martinsried, GERMANY
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Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZp434A014) is available at the RZPD in Berlin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at http://www.mips.biochem.mpg.de/proj/cDNA/
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Mammalia; Eutheria; Primates;
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DH10B; sites NotI + SalI"
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81 42	LeuTyrSerLeu 2 TGTACTCTTTG 8	LeuleuGlyaspMetTrpGlyargPheTrpThrasnLeuTyrSerLe 	rpGlyArgP GGGTAGAT	AspMetT: GATATGTO	euLeuGly TGCTTGGT	LeuProAlaHisI TCCCTGCTCATT	262 Let 	Оу	
61 82	ProlleGlyCys 2 CAATTGGATGC 7	AlaTyrValargalaLysLeuMetAsnalaTyrProSerTyrIleSerProIleGlyCy 	laTyrProS CCTATCCTT	MetAsna ATGAATG	lalysleu CAAAGTTG	aTyrValArg <i>a</i> CTATGTGAGGG	242 Ala 	Qy Db	
41 22	HUHISLEUHIS 2	LeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHis 	luGluIleL AAGAGATTA	ThrPheG:	alGluHis TGGAACAT	uIleGluAspV GATTGAAGATG	222 Let 663 TTC	Qy Db	
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01 02	\spTyrGlyAsp 2 ACTATGGGGAT 6	tAlaArgAlaAsnHisTyrGluAspTyrG 	laArgAlaA CAAGAGCAA	snGluMetAl \TGAGATGG(euLysAsn TGAAAAAT	luTyrValValLeuLysAs 	182 Glu 543 GAG	ОУ	
81	ProLeuTyrGlu 1	pGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyrG 	luvalGlyE AGGTCGGCA	ArgSerG] AGATCTG2	luSerTrp AAAGCTGG	euTrpAlaTrpG !TCTGGGCTTGGG	162 Leu 483 CTC	Qу	
61 82	YrAsnGluArg 1 ACAATGAGAGG 4	;luProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyr. 	lemetalaa: TAATGGCAA	AsnGluII AATGAAAI	roGlyLeu CAGGTTTG	euLeuLeuGluP ATTACTTGAAC	142 Leu 423 TTA	Qу	
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21 62	ThrIleLeuAsn 1 ACAATTCTAAAT 3	SerLysArgLeuAsnT AGCAAACGGTTGAACA	AG	euSerGluAspI CTCAGAAGAC <i>I</i>	GlySerSerValLeus GGGTCTTCAGTGCTCT	lnAsnGlySerS AAAATGGGTCTT	102 Glr 303 CAP	Qу	
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                                                                                                                                                                                                Baker.K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E., Gao,W.O., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K., Wood,W.L. and Zhang,Z.
                                                                                                                                                                                                                                                                                                Sequence 71 from Patent W00140466.
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160 TATCAAAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAATGTCCAA
CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln
                                       AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu
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                                                                                                                                                                                                                                                                                                            GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu
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       PF 22-JAN-1999 JP 1999014949

PR 13-MAY-1998 GB 9810373:2,18-AUG-1998 GB 9818009:4 PI
CHRISTOPHER D SAZAN, NICCLA BAGESU
PC C12N15/09,A61K31/00,A61K31/00,A61K31/00,A61K31/70,
PC A61K38/00,
PC A61K38/00,
PC A61K39/395,A61K45/00,A61K48/00,C07K14/47 ~~~~
PC G01N33/15,
PC G01N33/50 ~~~~~
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                                                                                  Eukaryota; Motazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2262)
Christopher, D.S. and Nicola, B.
MPROT15 polypeptide and MPROT15 polynucleotide
Patent: JP 199318472-A 2 24 NOV-1999;
SMITHKLINE BEECHAM CORP PUBLIC LTD CO
OS Homo sapiens (human)
PN JP 199918472-A/2
PD 24-NOV-1999 GB 9810373:2,18-AUG-1998 GB 9818009:4 PI
13-MAX-1998 GB 9810373:2,18-AUG-1998 GB 9818009:4 PI
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JP 1999318472-A/2.
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  C12R1:91),
A61K38/00,
A61K39/395,A61K45/00,A61K48/00,C07K14/47,C12P21/02,C12Q1/68.
G01N33/15,
G01N33/50,G01N33/50,G01N33/566,G01N33/68//(C12P21/02,
1:91), PC C12N15/00,
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Best Local Similarity:
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GluValGlyLysGlnLeuArgProLeuTyrGluGluTyrValValLeuLysAsnGluMet 190
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Location/Qualifiers
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/Organism="Homo sapiens"
/db_xref="taxon:9606"
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OTyrAlaAspGlnSerIleLysValArgIleSerLeuLysSerAlaLeuGlyAsp 630 ::: 1773	SerProTyr ::: AGTCCATGG	611 1765	Db Qy
eThrTrpLeuLysAspGlnAsnLysAsnSerPheValGlyTrpSerThrAspTrp 610 	LeuPheThr	591 1705	DP QA
nValValGlyAlaLysAsnMetAsnValArgProLeuLeuAsnTyrPheGluPro 590 	H — ₽	571 1645	Qу
nLysLeuPheAsnMetLeuArgLeuGlyLysSerGluProTrpThrLeuAlaLeu 570 	> - ₹	551 1585	Qy Db
aAlaLysHisGluGlyProLeuHisLysCysAspIleSerAsnSerThrGluAla 550	6 – A	531 1525	Db Qy
leArgTyrTyrThrArgThrLeuTyrGlnPheGlnPheGln 	rPheIl	7	D Qy
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$o {\tt HisAspGluThrTyrCysAspProAlaSerLeuPheHisValSerAsnAspTy}$	OHi	491	QУ
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etLeuThrAspProGlyAsnValGlnLysAlaValCysHisProThrAlaTrpAsp 350 	SerMetLe	331 1024	Qy Db
luLysPhePheValSerValGlyLeuProAsnMetThrGlnGlyPheTrpGluAsn 330 	AlaGluI GCCGAGA	311 964	ДЬ
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YArgPheTrpThrAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsn 290 	TrpGlyAr TGGGGTAG	271 844	ОУ

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KEYWORDS
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Sequence
AX047762
                                                                                                                                                                                                                                                                                                                                                            Zace2: a human metalloenzyme
Patent: WO 0070032-A 5 23-NOV-2000;
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Piddington, C.S., Petrie, C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                   ZymoGenetics,
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/protein_id="Cacl8992.1"
//protein_id="Cacl8992.1"
//db_xref="GI:11876769"
//db_xref="GI:11876769"
//db_xref="GI:11876769"
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//translation="MSSSSMLLISLVAVTTAQSFSLQEIQTPIIKRQLQALQQ
SGSSALSADKNKQLNTILNTMSTIYSTEKVCNEKNIPQECLLLEPGLDEIMATSTDYNS
RLMAWEGWRAEVGKQLRPLYEEVVLKNEMARANNYNDYGDYWRGDYEAEGADGYNNN
RNQLIEDVERTFABIKPLYEHLHAYVRRKLMDTYPSYISPTGCLPAHLLGDMWGRFWT
NLXPLTVPFAQKENIDVTDAMMNGGWDAERIFQEAEKFFVSVGLPHMTQGFWANSMLT
EPADGRKVVCHPTAWDLGHGDFRIKMCTKVTMDNFLTAHHEMGHIQZDMAYARQPFLL
RNGANEGFHEAVOEINGSLSAATFKHLKSIGLLPSDFQEDSETEINFLLKQALTIVGTL
PFTYMLEKWRMYVFRGEIPKEQMMKKWWEMKREIVGYVEPLHDETYCDPASLFHVSN
DYSFIRYYTRTIYQFQFQEALCQAAKYNGSLHKCDISNSTEAGQKLLKMLSLGNSEPW
TKALENVYGARNMDVKPLLNYFQPLFDWLKEQNRNSFVGWNTEWSPYADQSIKVRISL
KSALGANAYEWTNNEMFLFRSSVAYAMRKYFSIIKNQTVPFLEEDVRVSDLKPRVSFY
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                                                                                                                                                                                                                                                  /note="unnamed protein product"
                                                                                                                                                                                                                                                                                 /db_xref="taxon:10095"
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                  /organism="Mus sp."
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Patent WO0070032.
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                                                                                                                                                                                                                                                                                                                                                                                                   Shoemaker, K.E. and
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                                                                      ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640
                                                                                                                          AATTCTTTTGTGGGGTGGAACACTGAATGGAGCCCATATGCCGACCAAAGCATTAAAGTG
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consorthim/LINI at: http://image.llnl.gov Series: IRAK Plate: 31 Row: e Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF

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Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (04-APR-2002) National Institutes of Health, Mammalian Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Justitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Contact: MGC help desk
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Mus musculus, RIKEN cDNA 2010305L05 gene, clone MGC:25940
IMAGE:4236529, mRNA, complete cds.
                                                                                                                                      Sequencing Center
                                                                                                                                                         DNA Sequencing by: Baylor College of Medicine
                                                                                                                                                                                                                            Tissue Procurement: Jeffrey E. Green, M.D.
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GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu
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//translation="MSSSSWLLLSLVAVTTAQSITEENAKTFLNNFNOEAEDLSYQSS
//translation="MSSSSWLLLSLVAVTTAQSITEENAKTFLNNFNOEAEDLSYQSS
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RLWAWEGWRAEVGKQLRPLYEEYYVLKNEMARANNYNDYGDYWRGDYEAEGADGYNYN
RNQLLEDVERTFAEIKPLYEEHLHAYVERKLMDTYPSYISPTGCLPAHLLGDMWGREWT
NLYPLTVPFAOKFNIDVTDAMMNGGWDAERIFQEAEKFFVSVGLPHMTQGFWANSMLT
EPADGCRKVYCHPTAWDLGHGDFRIKMCTKVTMDNFLTAHHEMGHLQYDMAXARQPFLL
RNGANEGFHEAVGEIMSLSAATPKHLKKSIGLLPSDFQEDETEINFLLKQALTTVGTL
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DYSTIRVYTRTIVGPOFQEALCQAKKWEMKHENTSVGWNTEMSPYADQSIKVRISL
KSALGANAYENTNNEMELFRSSVAXAMKYESIKNOFVFLEEDVRVSDLKPKVSFY
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/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B"
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/protein_id="AAH26801.1"
/db_xref="GI:20071164"
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                                                                                                                                                                                                                                                          TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800
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carboxypeptidase, complete cds.
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Submitted (04-JAN-2001) Takami Komatsu, The insitute of medical science, Univesity of Tokyo, Laboratory of Genome Structure Analysis; 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
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247 ACCGAGGAAAATGCCAAGACATTTTTAAACAACTTTAATCAGGAAGCTGAAGACCTGTCT

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1446		Db
420	401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer	οv
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400	81 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe	Qy
1326	67 TGTACAAAGGTCACAATGGACAACTTCTTGACAGCCCATCACGAGATGGGACACATCC	DЪ
380	CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln	Qy
1266	07 AAAGTTGTCTGCCACCCCACAGCTTGGGAATCTGGGACACGGAGACTTCAGAATCAAGATG	Dβ
360	laValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet	Qγ
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340	21 ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln	Qy
1146	87 GGCTGGGATGCAGAAAGGATATTTCAAGAGGCAGAGAAATTCTTTGTTTCTGTTGGC	DЬ
320	rpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu	Qy
1086	7 TTGACTGTTCCCTTTGCACAGAAACCAAACATAGATGTTACTGATGCAATGATGAATCAG	Db
300	1 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln	Qy
1026	7 TGCCTCCCTGCCCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACCCT	Db
280	CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer	Qy
966	7 CATGCCTATGTGAGGAGGGAGTTGATGGATACCTACCCTTCCTACATCAGCCCCACTGGA	Дb
260	HisalaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly	Qy
906	7 CAGTTGATTGAAGATGTAGAACGTACCTTCGCAGAGATCAAGCCATTGTATGAGCATCTT	Дb
240	GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu	Qy
846	GATTATTGGAGAGGGGACTATGAAGCAGAGGGAGCAGATGGCTACAACTATAACCG	Дb
220	l AspTyrTrpArgGlyAspTyrGluValAsnGlyV	Qy
786	GAAGAGTATGTGGTCCTGAAAAACGAGATGGCAAGAGCAAACAATTATAACGACTATGG	DЬ
200	GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHi	Qy
726	AGGCTCTGGGCATGGGAGGGCTGGAGGCTGAGGTTGGCAAGCAGCTGAGGCCGTTGTA	Db
180	LeuTrpAlaTrpGluSerTrpArgSerGluV	Qy
666	TGCTTATTACTTGAGCCAGGATTGGAATAATGGCGACAAGCACAGACTACAA	р
	CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 1	Qy
606	TTACAGTACTGGAAAAGTTTGCAACCCAAAGAACCCACAAGAA 6	Db
40	21 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 1	Qy
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20	01 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 1	Qy
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00	lnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu 1	Qy

800 pValGlnThrSerPhe 805	Qy
781 TyralaSer-IleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAs 	y Ag
761 ilePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsn	Qy db
741 IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIle	Qy Db
721 SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValS	Qy Db
701 GluLysalaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAs 	Qу Db
681 PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVa ::: ::: :::	Qy Db
661 GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleS	Qy Db
641 TyrleuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysA::::	Оу
621 ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluM 	Qy Db
601 AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysV 	Qy Db
581 ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLy	Qy Db
561 GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAs 	Фр
541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 	Фр
521 TyrGinPheGinPheGinGluAlaLeuCysGinAlaAlaLysHisGiuGlyProLeuHi 	Фy
501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLe 	Фу
481 LysargGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPr 	Qy Db
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                                                               AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80
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Patent: WO 0070032-A 8 23-NOV-2000;
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GCTCAGACTTCCTTT 2520
                                                                      TATGACTCGATGGACATTGGAAAAGGAGAAAGCAATGCAGGATTCCAAAACAGTGATGAT
                                                                                          TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800
                                                                                                                                                 ATTGTCACTGGGATCAAAGGTCGAAAGAAGAAAAATGAAAACAAAAAGAGAAGAACCCT
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181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly
                                481 MGNYTNTGGGCNTGGGARWSNTGGMGNWSNGARGTNGGNAARCARYTNMGNCCNYTNTAY 540
                                                                                                                                                               361 AAYACNATGWSNACNATHTAYWSNACNGGNAARGTNTGYAAYCCNGAYAAYCCNCARGAR
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                                                                                                                              CysLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160
                                                             ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180
                                                                                               TGYYTNYTNYTNGARCCNGGNYTNAAYGARATHATGGCNAAYWSNYTNGAYTAYAAYGAR 480
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Sequence 3 from Patent W00070032.
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1. .2415
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218 c 398 g
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/db_xref="taxon:32630"
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                                                                                                                                                                                  501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                 441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661 CARYTNATHGARGAYGTNGARCAYACNTTYGARGARATHAARCCNYTNTAYGARCAYYTN 720
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                                                                                      TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540
                                                                                                                                                                                                                                                                                                                                   TGGATGGTNTTYAARGGNGARATHCCNAARGAYCARTGGATGAARAARTGGTGGGARATG 1440
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Search completed: March Job time : 4946 secs 7, 2003, 09:08:57

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SUMMARIES

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Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-Q-Cgn2_1/USPTO_Spool_VG09978385/runat_28022003_104716_1332/app_query.fasta_1.967
-DB=N_Geneseq_101002 -QPMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40 cdi
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40 cdi
-LST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MXX=100 -THR_MIN=0 -ALIGN=20
-MODE=LOCAL -QUTFMT=pto -NORM=ext -HEASSIZE=500 -MINLEN=2000000000
-USER=US09978385_@CGN_1_1_396_@runat_28022003_104716_1332 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-NARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                           Homo sapiens.
                                                                                                                                                                               Human MPROT15 coding sequence #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 14; 22pp; Japanese.
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Zace2 gene in a biological sample, as probes for in vivo diagnosis and for detecting and localizing Zace2 gene expression in tissue samples, to determine whether a subject's chromosomes contain a mutation in the Zace2 gene, and to detect aberrations associated with the Zace2 locus. Inhibitors of ACE are used for treating hypertension of various conditions, including left ventricular systolic dysfunction, progressive renal impairment, scleroderma renal crisis, congestive heart failure due to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be used to treat infertility while Zace2 antagonists are used for inducing infertility. The present sequence represents a cDNA encoding the human
                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-converting enzyme is a zinc metallopeptidase that plays roles in blood pressure regulation and fertility. Zace2 can be expressed by standard recombinant methodology. Zace2 polypeptides are useful for treating an inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), diseases associated with inflammation like arthritis and entercoolitis, as targets for identifying modulators of zinc protease activity, for screening or identifying new angiotensin-converting enzyme (ACE) inhibitors, and as a basis for rational drug design for inhibitory molecules. The nucleic acids can be used to detect the expression of a converting enzyme in the converting enzyme i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Angiotensin-converting enzyme, Zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases associated with inflammation such as arthritis and enterocolitis -
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Alignment Scores:

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Percent Similarity:

Percent Similarity:

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Best Local Similarity:

100.00%

Mismatches:

Ouery Match:

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DB:

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Length:

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Matches:

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Monservative:

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Mismatches:

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Gaps:

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US-09-978-385-2 (1-805) x AAC84366 (1-3334)

Qy	Db	Qγ	Db	Qy	Db	Qy	
61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla 80	155 TATCAAAGTTCACTTGCTTCTTGGAATTATAAACACCAATATTACTGAAGAGAATGTCCAA 214	41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60	95 ATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC 154	21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40	35 ATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACC 94	1 MetSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20	

Qy 781 TyralaSerIleAspIleSerL	Qy 761 IlePheThrGlyIleArgAspA	Qy 741 IleTrpLeuIleValPheGlyV	Qy 721 SerLeuGluPheLeuGlyIleG 	Qy 701 GluLysalaIleArgMetSerA	Qy 681 PheAsnPhePheValThrAlaP	Qy 661 GlnMetIleLeuPheGlyGluG 	Qy 641 TyrLeuPheArgSerSerValA	Qy 621 ArgIleSerLeuLysSerAlaI	Qy 601 AsnSerPheValGlyTrpSerT	Qy 581 ValargProLeuLeuAsnTyrE 	Qy 561 GlyLysSerGluProTrpThrI	Qy 541 LyscysaspileSerAsnSerT	21 1 95 1	Qy 501 AlaSerLeuPheHisValSerA	Oy 481 LysArgGluIleValGlyValV	Qy 461 TrpMetValPheLysGlyGlul	Qy 441 LysGlnalaLeuThrIleValQ
YrālaSerīleAspīleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800 	IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro 780 	IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIIleLeu 760 	SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740 	lluLysalaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn 720 	hePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal 700 	lnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer 680 	YrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn 660 	ArgIleSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet 640 	\snSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal 620	ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600 	GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 580 	.eSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeu 560 	YrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540 	.laSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520 	<pre>xrgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500 </pre>	rpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480 	.eValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460

440	421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu « 	Qy
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111	1055 AAAGCAGTCTGCCATCCCACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATG	B 5
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9 1	935 GCCTGGGATGCACAGAGAATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTT	B 1
	875 TTGACAGTTCCCTTTGGACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAG	D D
87 ₄	815 TGCCTCCCTGCTCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCT 281 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln	δ B
280	261 CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer	γQ
260	241 HisalaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly	B 6
75.	695 CAGTTGAAGATGTGGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTT	망
694	635 GATTATTGGAGAGGAGACTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGGC	ον σα
220	201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly	δÕ
200	181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 	DP GA
180	161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr	D dg
51,	455 TGCTTACTTGAACCAGGTTTGAATGAATAATAGGCAAACAGTTTAGACTACAATGAG	문 5
4.5	395 AATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAA	문
140	121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu	γQ
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27.		Db

US-09-978-385-2 (1-805) x AAA12764 (1-3396)

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RESULT 3
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                                                             Local Similarity:
                                                                                                                                                                                                                                                                                        The present sequence encodes a human angiotensin converting enzyme-2 (ACE-2). ACE-2 is expressed predominantly in kidneys and testis. The sequence of the full length ACE-2 CDNA was determined from a clone obtained from a CDNA library prepared from mRNA of a human heart of a subject who had congestive heart failure. ACE-2 has significant sequence homologies with ACE enzymes, and has also been shown to hydrolyse angiotensin I into Ang.(1-9). The ACE-2 therapeutics are used to treat blood pressure related diseases and conditions, such as hypertension, congestive heart failure, chronic heart failure, acute heart failure, myocardial infarction, atherosclerosis and renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 1; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid encoding angiotensin converting enzyme-2 (AC polypeptide useful for detecting an ACE-2 therapeutic for treating hypertension, congestive heart failure, myocardial infarction,
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                                                                                      CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer
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AAAGCAGTCTGCCATCCCACAGCTTGGGACCTGGGGAAGGGCCACTTCAGGATCCTTATG
                                           CCTAATATGACTCAAGGATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAG
                                                     ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln
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GluLysalaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsn
                                                 GTAAGGCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAG
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                              PheAsnPhePheValThrAlaProLysAsnValSerAspIleIleProArgThrGluVal
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                      TTTAATTTCTTTGTCACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTT
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              Claim 1;
                              screening
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                                              Novel
                                                              P-PSDB;
                                                                                     Acton
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                                                                                                                   11-DEC-1997;
                                                                                                                                  11-DEC-1997;
                                                                                                                                                  27-FEB-2001
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                                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                      sig_peptide
                                                                                                                                                                                                                                                                                                                 inflammation;
                                                                                                                                                                                                                                                                                                                         screening;
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                                                                                   SL,
                                genes encoding angiotensin ense or antigene agents for ning assays -
                                                                                                                                                                                                                                                                                                                        angiotensin converting enzyme-2; ACE-2; pept
ing; therapy; hypertension; congestive heart
                                                                                                    MILLENNIUM PHARM INC
              Fig 1; 76pp;
                               assays
                                                                                                                                                                                                                                                                                                                 therapy; on; pain;
                                                                                    Robison
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136..2496
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/note= "This region is referred

specifically claimed in claim 26

82...135
                                                                                                                                                                                /*tag= c
/product=
(ACE-2)"
                                                                                                                                                                                                                                                  /*tag= a
/product= "Human angiotensin converting
(ACE-2)"
                                                                                                                                                                                                                                                                          Location/Qualifiers 82..2499
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                                      converting enzyme-2 useful therapeutics, diagnostics a
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eart failure; CHF;
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CDNA. ACE is also referred as peptidyl dipeptidase A. Nucleic acid sequence encoding ACE-2 is useful as antisense or antigene agents for sequence specific modulation of gene expression or in the analysis of single base-pair mutations in the gene. Nucleic acid sequence encoding ACE-2 is useful in therapeutics, diagnostics and in screening assays. ACE-2 antagonist is used to treat hypertension or congestive heart failure (CHF). ACE agonist is used to reduce the inflammation and pain resulting from an insect sting or bite, which was accompanied by an injection of bradykinin. Anti-ACE-2 antibodies are used to monitor ACE-2 protein levels for determining the disease or condition associated with an aberrant protein level.
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Qy	Db Qy	DЬ	do Qy	QУ	Db 04	Db Qy	Дb	Оу	DB Qy	D Q	DB Qy	ОУ	US-0	Align Pred. Score Perce Best Query DB:	3555555555555555
241 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrTleSerProIleGly 260	221 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240 	201 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220 	181 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly 200 	161 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr 180 	141 CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 160 	121 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140 	101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120 	81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu 100 	61 ASDMetASDASDASDASDLYSTTpSerAlaPheLeuLySGluGlnSerThrLeuAla 80 	41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60 	21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40 	1 MetSerSerSerSrTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20 	9-978-385-2 (1-805) x AAD02758 (1-3396)	nment Scores: 0 Length: 3396 e: 4291.00 Matches: 805 ent Similarity: 100.00% Conservative: 0 Local Similarity: 100.00% Mismatches: 0 y Match: 100.00% Indels: 0 Gaps: 0	CDNA. ACE is also referred as peptidyl dipeptidase A. Nucleic acid sequence encoding ACE-2 is useful as antisense or antigene agents for sequence specific modulation of gene expression or in the analysis of single base-pair mutations in the gene. Nucleic acid sequence encoding ACE-2 is useful in therapeutics, diagnostics and in screening assays. ACE-2 antagonist is used to treat hypertension or congestive heart failure (CHF). ACE agonist is used to reduce the inflammation and pain resulting from an insect sting or bite, which was accompanied by an injection of bradykinin. Anti-ACE-2 antibodies are used to monitor ACE-2 protein levels for determining the disease or condition associated with an aberrant protein level.

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      muscle mass; body fat; obesity; diabetes; atherosclerosis; weight loss; lipid metabolism; weight gain; anorexia; cachexia; bulimia; sepsis; familial partial lipodystrophy; hypercholesterolaemia; hyperlipidaemia; aberrant metabolic rate; heart failure; left ventricular hypertrophy; neurodegenerative disorder; peptide hormone; cytokine processing; myocardial infarction; cardiomyopathy; inflammatory bowel disease; systemic inflammation response syndrome; polytrauma; pain; stroke; bone destruction; rheumatoid arthritis; osteoarthritis; asthma; periodontal disease; dysmenorrhoea; premature labour; brain oedema; focal injury; diffuse axonal injury; reperfusion injury; scar formation; subaracchnoid haemorrhage; allergic disorder; adult respiratory distress syndrome; wound healing; appetite;
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                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding human angiotensin converting enzyme-2 (ACE-2) protein.
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    "Human angiotensin converting enzyme-2 (ACE-2)
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                                                                                                                                                                                                                                                                                                                                            CC The present invention describes a new method of treating a body weight CC disorder, increasing muscle mass and decreasing body fat by CC administration of angiotensin converting enzyme (ACE)-2 modulating CC compound. The invention can be used for treating body weight disorders, CC particularly obesity of at least grade 1, diabetes, atherosclerosis and CC a state associated with lipid metabolism. The method is used for treating CC rapid weight loss, rapid weight gain, anorexia, cachexia, bulimia, CC generalised partial lipodystrophy, familial partial lipodystrophy, CC hypercholesterolaemia, hyperlipidaemia, an aberrant metabolic rate, CC congestive heart failure, chronic heart failure, left ventricular CC hypertrophy, acute heart failure, neurodegenerative disorders (e.g. CL alzheimer's disease, Parkinson's disease and Huntington's disease), CC Mizheimer's disease, Parkinson's disease and Huntington's disease, CC myocardial infarction, cardiomyopathy, systemic inflammation response CC syndrome, sepsis, polytrauma, inflammatorid arthritic and actor arthritic
                                                                                                                                                                                chronic pain, bone destruction in rheumatoid arthritis and osteoarthritis and periodontal disease, dysmenorrhoea, premature labour, brain oedema following focal injury, diffuse axonal injury, stroke, reperfusion injury, cerebral vasospasm after subarachnoid haemorrhage, allergic disorders including asthma, adult respiratory distress syndrome, wound healing and scar formation. The invention decreases the appetite, increases muscle mass and decreases body fat of subject having body mass index of greater than 23 (preferably 24.9)kg/m^2. The present nucleic acid sequence encodes the human ACE-2 protein of the invention.
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29-MAY-2001; 2001US-0870382
19-OCT-2001; 2001US-371741P
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                                                                                                                                                Sequence 3396 BP; 1034 A; 659 C;
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1281		1222	Db
380 1221	CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln:	361 1162	Db Qy
360	LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet	341	dg
1161		1102	VQ
340 1101	ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln :	321 1042	Db Qy
320 1041	AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu :	301 982	Дb
300	uThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln	281	Оy
981		922	
280 921	CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer :	261 862	Db Qy
260 861	nAlaTyrProSerTyrIleSerProIleGly GCCTATCCTTCCTATATCAGTCCAATTGGA	241 802	Оy
240	ValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu	221	Дy
801		742	
220	ASPG1YTYrASPTYrSerArgG1y	201	dd Qy
741		682	
200	alleuLysasnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly	181	рь
681		622	
180	GluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr	161	oy
621		562	bb
160	uGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu	141	dq
561		502	dy
140	IleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu	121	Оy
501		442	
120 441	GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu :	101 382	Db Qy
100 381	GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu :	81 322	Оу
80 321	AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla (61 262	Db Qy
60	TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln (41	Qy
261		202	Db

40. HISCHARGETTICTGGGAANCHUTTERAGAGACHACHTICTCAGCCCCCAGCAGACHAGATICTCAGCAGACHAGACHTICTGAGCAGACHAGACHTICTGAGCAGCACACAGACHAGACHTAGCAGATTAGAGCAGCAGCACAGAGACHAGACH	780	1 IlePheThrGlyIleArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnPro	76	Qy
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#UL HISCLINA'S WILL'S LILLIENE CENTRALATION OF STILLIES LINES 12	w		24	Db
#10 Institutional Control Institution Institutional In	4	SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSe	N	Qy
#10 INSCRIPTION OF CONTROL OF THE PROPERTY O	N		18	Db
#01 HSGLULLEWSCEPTOAGGGAANTCATGTCACTTACTAGARGTTTTCOAGGACTACCATTTACAACTGCTTCATGAGACTGCACTTTCAGAGCCGCACCCTAGACTTACAATTCC 14 421 TIGGIYEULEWSETPTOAGASPHAGINABAGAGATGAAACGAAATTAAACTCC 14 422 TIGGIYETCTCCCCCATTTTCAGAAGAGACAATGAAACGAAATAAACTCCTCCTGCTC 14 1342 ATTGGTCTTCTCCCCCATTTTCAGAAGAGACAATGAAACGAAATAAACTCCTCCTGCTC 14 1342 ATTGGTCTTCTCACCCCATTTTCAGAAGAGACAATGAAACAAAAAAAA	Ñ	. GluLysAlaIleArgMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAs	0	Qγ
1	-	TTTAATTTCTTTGTCACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGT	12	Db
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118-118-118-118-118-118-118-118-118-118	0	ValargProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLy	00	Qy
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401 HISGIDAIAVALOTYGILLIEMENSETALANSETALARTEFICOYSHISHCULYSSET 42	ن.	AAGCGAGAGATAGTTGGGGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCC	Ñ	망
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401 HISGIDAIAVAIOLYGIDLIEMECSETLEUSETALATATTFFOOYSHISLEULYSSET 42	œ	TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMe	6	Qу
401 HISGIDA AVAIDA SELLEMENSERIA BERTALISTRA DA SELLA LINE PLONGS HISBEULLYSSER 42	4	AAACAAGCACTCACGATTGTTGGGACTCTGCCATTTACTTAC	40	Db
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AND USON THE PROPERTY OF THE P	420	isGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSe	40:	Qγ

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GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly
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The invention relates to human angiotensin converting enzyme-2 (ACE-2) polypeptides and polynucleotides. ACE-2 is also known as peptidyl dipeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for treating or preventing the development of abnormal blood pressure and diseases or disorders associated with the protein in a subject. The diseases include hypertension, hypotension, congestive heart failure, chronic heart failure, acute heart failure, myocardial infarction, atherosolerosis, arrhythmia and renal failure. They are also useful for treating inflammatory conditions and diseases relating to fertility. The present sequence is human full-length ACE-2 cDNA. The ACE-2 gene is located on the X chromosome at p21-22.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:

US-09-978-385-2 (1-805) x AAD32586 (1-3396)

621	562 AGGCTCTGGGCTTGGGAAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATAT (Db
180	٠,	Qy
561		Db
160	141 CysLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu 1	Qy
501	442 AATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAA	Дb
140		Qy
441	382 CAGCAAAATGGGTCTTCAGTGCTGTCAGAAGACAAAAGGGCAAACGGTTGAACACAATTCTA	Db
120		Qy
381	322 CAAATGTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTT	В
100	_	Qy
321	262 AACATGAATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCC	Db
80		Qy
261	202 TATCAAAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAA	Db
60		Qy
201	142 ATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC	Db
40		Qy
141	82 ATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGTTGCTGACTGCTCCTCAGTCCACC 1	Db
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Pred. No.:
                                        Alignment Scores:
                                                                                                                 CC PRO polypeptides, and to detect the presence of mammalian lung, colon, cc breast, prostate, rectal, cervical or liver tunours by comparing PRO polypeptide expression in a cell sample to that in a control sample. CC some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor alpha (TNF-alpha) from human blood, the crowdifferation or differentiation of chondrocytes, the proliferation or cc gene expression in pericyte cells, the release of proteoglycans from cc cartilage, the proliferation of inner ear utricular supporting cells or cf T-lymphocytes, the release of a cytokine from peripheral blood cc monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify comolecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, cc transgenic or knock out animals and can be used in gene therapy.
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PRO
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                                                                                   Sequence
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Tumas
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A, Godowski PJ, Gurney AL, Sherwood S;
Tunas D, Watanabe CK, Wood WI, Zhang Z
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                                                                                   821 G; 1052 T; 0 other;
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                       ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln
                                                                  GCCTGGGATGCACAGAGAATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTT
                                                                                                                                                                                        LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACATGAATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln
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Ġ i	1540 GCATCTCTGTTCCATGTTTCTGATGATTACTCATTCGATATTACACACAGGACCCTT	DЬ
20	501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThr	Qy
G (1480 AAGCGAGAGATAGTTGGGGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCC	Db
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400	381 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGly	νQ
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380	361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlvHisIl	δÕ
⊢ (1060 AAA	Dβ
2 C	341 LysAlaValCysHisProThrAlaTrpAspLeuGlvIvsGlvAspPhaArcTlot	γQ
1059	b 1000 CCTAATATGACTCAAGGATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTCAG	망

Qy	<u> </u>
DЬ	39 TGGACCCTAGCATTGGAAAATGTTGTAGGAGC-AAGAACATGAATGTAAGGC
Qy	LeuPheThrTrpLeuLysAspGlnAsnLysAsnSerPheValG
Db	ACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTCTTTTGTGGG
Qy	rpSerThrAspTrpSerProTyrAlaAsp-GlnSerIleLysValArgIleSerLeuLy 6
рь	w
Qy	laLeuGlyAspLysAlaTyrGluTrp
Db	2318 ATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATC 2377
Qy	SerValAlaTyrAlaMetArgGlnTyrPhe
Db	2378 ATCTGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTT 2437
Qy	GluGluAspValArgValAlaAsnLeuLysProArgIleSerPheAsnPhePheV
Db	GGGGAGG
Qy	AlaProLysAsnValSerAspIleIleProArgThrGluValGluLysAlaIleA
Db	ACTG
Qy	MetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPhe
Db	GTCCCGG
Qy	725 uGlyIleGlnProThrLeuGlyProProAsnGlnProProValSerIleTrpLeuIleVa 745
DЬ	GGATACAGCCAACACTTGGACCTCCTAACCAGCCCCTGTTTCCATATGGCTGATT
Qy	ValIleLeuIlePheThrGlyI
Db	78 TTTTGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATC
Qy	rGlyGluAsnProTyrAlaSerIleA
Db	AGAGATCGGAAGAAAAATAAAGCAAGAAGTGGAGAAATCCTTATGCCTCC
Qy	eSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAspValGlnThrSer
₽	ATTAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGATGTTCAGACCTCCT
Qy	805 e 805
Db	2858 T 2858
RESUL AAS14 ID	LT 8 4880 AAS14880 standard; cDNA; 2920 BP.
X AC	AAS14880;
X D	20-DEC-2001 (first entry)
XX	an cDNA encodin
X X X	Human; novel human protein; NHP; ss; antidiabetic; antirheumatic; antiarthritic; cytostatic; antiarteriosclerotic; vulnerary; neuroprotective; nootropic; antiparkinsonian;
K W	i-human immunodeficiency virus; antiasthmatic; vasotropic; otensive; anorectic; antiinfertility; neuroleptic; anticon
X X W	<pre>imanic; immunosuppressive; cerebroprotective; antimicrobial; iinflammatory; antibacterial; antipsoriatic; thyronimetic.</pre>
KW	unomodulator; antiseborrheic; dermatological; vas trointestinal disorder; cardiovascular disorder;
KW	onary heart disease; arteriosclerosis; anorexia; obesity; bul

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CC involving vasoconstriction, gastrointestinal disorders, cardiovascular CC disorders (e.g. hypertension, erectile dysfunction, high blood pressure, CC coronary heart disease and arteriosclerosis), anorexia, obesity, bulimia, CC cachexia, disorders of small intestine, disorders of reproductive system CC cachexia, disorders of small intestine, disorders of reproductive system CC cachexia, disorders, lang tumours CC and other hyperproliferative disorders, disorders of pulmonary system, CC disease, huntington's disorders, disorders of pulmonary system, CC disease, Huntington's disease, schizophrenia, mania, dementia, paranoia, parchase, autism, sleep disorders (e.g. Alzheimer's disease, Parkinson's CC psychoses, autism, sleep disorders), immune system disorders (e.g. grain injury and/or stroke), infectious disease, diabetes mellitus, cC parin finjury and/or stroke), infectious diseases, diabetes mellitus, cC immunological disorders (e.g. asthma, acquired immunodeficient syndrome CC (AIDS), leukaemia, rheumatoid arthritts, inflammatory bowel disease, sepsia, acne, psoriasis and lupus erythematosus), neural system disorders, respiratory disorders, olianoters and wound disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huntington's disease; schizophrenia; mania; dementia; paranoia; panic disorder; learning disability; amyotropic lateral sclerosis; psychosis; autism; sleep disorder; immune system disorder; Hashimoto's thyroiditis; musculo-skeletal system disorders; multiple sclerosis; ischaemic brain injury; stroke; infectious disease; diabetes mellitus; immunological disorder; asthma; AIDS; acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis; inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus; neural system disorder; respiratory disorder; olfactory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cachexia; male infertility; impotence; testicular cancer; lung tumour; hyperproliferative disorder; pulmonary system disorder; central nervous system disorder; bone disorder; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acids that encode them and antibodies raised against them. The proteins, antibodies and nucleic acids are useful in the diagnosis, prognosis, prevention and/or treatment or diseases and/or disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human proteins, useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cardiovascular disorders, autoimmune disorders and reproductive disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-2001; 2001WO-US10542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 291-292; 318pp; English.
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healing. The present sequence encodes an NHP is located on the X chromosome.
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2000US-236384P.
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/trans1_except= (pos:867..869,aa:Xaa)
/trans1_except= (pos:930..932,aa:Xaa)
/trans1_except= (pos:1707..1709,aa:Xaa)
/note= "Xaa= Any amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 tAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAlaGlnMe
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                                                                                                                                                                                uIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeuHisAl
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                                                                   uProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSerLeuTh
                                                                                                                                                                                                                                                                                               uTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyrGluGl
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AGTTCCCTTTGGACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAGRCCTG
                                                                                                           aTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGlyCysLe
                                                                                                                                                                 GATTGAAGATGTGGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTTCATGC
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             rValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGlnAlaTr
                                                      CCCTGCTCATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAAATYTGTACWSTTTGAC
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tIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSerPheAs 682
                                               uPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsnGlnMe 662
                                                                                                                                                                 eSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLe
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                                                                                                                                    AAGCCTAAAATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9GluIleValGlyValValGluProValProHisAspGluThrTyrCysAspProAlaSe 502
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11-OCT-2001. WO200174896-A1.

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Location/Qualifiers 213..998 /product= "NHP #11"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huntington's disease; schizophrenia; mania; dementia; paranoia; panic disorder; learning disability; amyotropic lateral sclerosis; psychosis; autism; sleep disorder; immune system disorder; Hashimoto's thyroiditis; musculo-skeletal system disorders; multiple sclerosis; ischaemic brain injury; stroke; infectious disease; multiple sclerosis; ischaemic brain injury; stroke; infectious disease; diabetes mellitus; immunological disorder; asthma; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acquired immunodeficient syndrome; leukaemia; rheumatoid arthritis; inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus; neural system disorder; respiratory disorder; olfactory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antimanic; immunosuppressive; cerebroprotective; antimicrobial; antiinflammatory; antibacterial; antipsoriatic; thyromimetic; immunomodulator; antiseborrheic; dermatological; vasoconstriction; gastrointestinal disorder; cardiovascular disorder; hypertension; coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hyperproliferative disorder; pulmonary system disorder; central nervous system disorder; bone disorder; neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cachexia; male infertility; impotence; testicular cancer; lung tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypotensive; anorectic; antiinfertility; neuroleptic; anticonvulsant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuroprotective; nootropic; antiparkinsonian;
anti-human immunodeficiency virus; antiasthmatic; vasotropic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarthritic; cytostatic; antiarteriosclerotic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA encoding novel human protein NHP #11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          healing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC disorders (e.g. hypertension, erectile dysfunction, high blood pressure, cc coronary heart disease and arterioscierosis), anorexia, obesity, bulimia, cc cachexia, disorders of small intestine, disorders of reproductive system cc (e.g. male infertility and/or impotence), testicular cancer, lung tumours cc and other hyperproliferative disorders, disorders of pulmonary system, cc entral nervous system disorders, bone disorders, neurodegenerative cc diseases and behavioural disorders (e.g. Alzheimer's disease, Parkinson's cc disease, Huntington's disease, Schizophrenia, mania, dementia, paranoia, cc panic disorder, learning disabilities, amyotropic lateral sclerosis, cc psychoses, autism, sleep disorders), immune system disorders (e.g. central nervous system disorders), immune system disorders, cc thanhimoto's thyroiditis), renal and musculo-skeletal system disorders, communological disorders (e.g. amultiple sclerosis, isohaemic cc immunological disorders (e.g. asthma, acquired immunodeficient syndrome cc (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease, cc sepsis, acne, psoriasis and lupus crythematosus), neural system disorders, respiratory disorders, olfactory disorders and wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel human proteins (NHP) and the nucleic acids that encode them and antibodies raised against them. The proteins, antibodies and nucleic acids are useful in the diagnosis, prevention and/or treatment or diseases and/or disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human proteins, useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cardiovascular disorders, autoimmune disorders and reproductive disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2911 BP; 896 A; 570 C; 655 G; 788 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 297-298; 318pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             healing. The present sequence encodes an NHP of the invention
                         102 nAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeuAsnTh 122
                                                                                                                                                                                                                                                                  155
                                                                                                                    82
                                                                                                                                                                                              62 tAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAlaGlnMe 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThrIleGlu 22
                                                                      GTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCA
                                                                                                                  tTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeuGlnGl 102
                                                                                                                                                                  GAATAATGCTGGGGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCCCAAAT 274
                                                                                                                                                                                                                                                                     AAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACAT 214
                                                                                                                                                                                                                                                                                              nSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGlnAsnMe 62
                                                                                                                                                                                                                                                                                                                                                                GAACAGGCCAAGACATTTTTGGGACAAGTTTAACCACGAAGCCGAAGACCTGTTCTATCA 154
                                                                                                                                                                                                                                                                                                                                                                                                             GluGlnAlaLysThrPheLeu-AspLysPheAsnHisGluAlaGluAspLeuPheTyrGl 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCTCTTCCTGGCCTCCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACCATTGAG
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                                                                                                                                               442 nAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArgTrpMe 462
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MPROT15; treatment; hypertension; human; myocardial disease;
heart disease; apoplexy; heart disease; nervous denaturation;
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                                       Human MPROT15 coding sequence
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                                                                                                                                                                                                                                                                                                                                                                        TTTCTTTGTCACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAA
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is coding sequence #2 of human MPROT15. The MPROT15 polynucleotide and polypeptide sequences can be used for the treatment of hypertension, myocardial diseases, apoplexy, heart diseases, nervous denaturation, Alzheimer's disease and diseases related to the processing of peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPROT15 polypeptide and MPROT15 polynucleotides - useful itreatment of hypertension, myocardial diseases, apoplexy, diseases, nervous denaturation, Alzheimer's disease etc.
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18-AUG-1998;
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IleMetAlaAsnSerLeuAspTyrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSer 170
                            LeuThrValLysLeuGlnLeuGlnAlaLeuGlnGlnAsnGlySerSerValLeuSerGlu
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                                                                                   AspLysSerLysArgLeuAsnThrIleLeuAsnThrMetSerThrIleTyrSerThrGly
                                                                                                                 CTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTCAGTGCTCTCAGAA
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530	SerPheIleArgTyrTyrThrArgThrLeuTyrGlnPheGlnPheGlnGluAlaLeuCys	511	Qy
147		1476	망
510	ValProHisAspGluThrTyrCysAspProAlaSerLeuPheHisValSerAsnAspTyr	491	Qy
147	GACCAGTGGATGAAAAGTGGTGGGAGATGAAA	1444	DЬ
490	AspGlnTrpMetLysLysTrpTrpGluMetLysArgGluIleValGlyValValGluPro	471	QУ
144	CATTTACTTACATGTTAGAGAAGTGGAGGTGGATGGTCTTTAAAGGGGAAATTCCCAAA	1384	Дb
470	ProPheThrTyrMetLeuGluLysTrpArgTrpMetValPheLysGlyGluIleProLys	451	Qy
1383	GACAATGAAACAGAAATAAACTTCCTGCTCAAACAAGCACTCACGATTGTTGGGACTCTG	1324	В
450	AspAsnGluThrGluIleAsnPheLeuLeuLysGlnAlaLeuThrIleValGlyThrLeu	431	Qy
1323	TCTGCAGCCACACCTAAGCATTTAAAATCCATTGGTCTTCTGTCACCCGATTTTCAAGAA	1264	Ъ
430	SerAlaAlaThrProLysHisLeuLysSerIleGlyLeuLeuSerProAspPheGlnGlu	411	Qy
1263	CTGCTAAGAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGGAAATCATGTCACTT	1204	Db
410	LeuLeuArgAsnGlyAlaAsnGluGlyPheHisGluAlaValGlyGluIleMetSerLeu	391	Qy
1203	ACAGCTCATGAGATGGGGCATATCCAGTATGATATGCTATATGCTGCACAACCTTTT	1144	DЬ
390	ThrAlaHisHisGluMetGlyHisIleGlnTyrAspMetAlaTyrAlaAlaGlnProPhe	371	QΥ
1143	CTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAATGGACGACTTCCTG	1084	рb
370	LeuGlyLysGlyAspPheArgIleLeuMetCysThrLysValThrMetAspAspPheLeu	351	Qy
1083	TCCATGCTAACGGACCCAGGAAATGTTCAGAAAGCAGTCTGCCATCCCACAGCTTGGGAC	1024	Ъ
350	SerMetLeuThrAspProGlyAsnValGlnLySAlaValCysHisProThrAlaTrpAsp	331	Qy
1023	GCCGAGAAGTTCTTTGTATCTGTTTGGTCTTCCTAATATGACTCAAGGATTCTGGGAAAAT	964	망
330	AlaGluLysPhePheValSerValGlyLeuProAsnMetThrGlnGlyPheTrpGluAsn	311	Ϋ́
963	ATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGGATGCACAGAGAATATTCAAGGAG	904	DЪ
310	IleAspValThrAspAlaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGlu	291	Qy
903		844	망
290	${\tt TrpGlyArgPheTrpThrAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsn}$	271	Qγ
843	GCCTATCCTTATATCAGTCCAATTGGATGCCTCCCTGCTCATTTGCTTGGTGATATG	784	ф
270	AlaTyrProSerTyrIleSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMet	251	Qy
783	GAAGAGATTAAACCATTATATGAACATCTTCATGCCTATGTGAGGGCAAAGTTGATGAAT	724	В
U	GluGluIleLysProLeuTyrGluHisLeuHisAlaTyrValArgAlaLy	231	Qy
Ν	JACTACAGCCGCGGCCAGTTGATTGAAGATGTGGA	64	В
230	lyValAspGlyTyrAspTyrSerArgGlyGlnL		QΥ
6		04	Вb
۱.	laargalaasnHisTyrGluaspTyrGlyaspTyrTrpargGlyaspTy	91	γQ
603		44	₽b '
190	luValGlyLysGlnLeuArgProLeuTyrGluGluTyrValValLeuLysAsnGlu	71	VΩ

antiarthritic;

bradykinin inactivator; ss.

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                                                 zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility; zinc metallopeptidase; blood pressure; zinc metallopeptidase; blood pressure; zinc metallore; pertension; ventricular systolic dysfunction; renal impairment; heart failure; scleroderma renal crisis; atherosclerosis; antiinflammatory; mouse;
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                                                                                                                                                                                                                                                                                                                                                              GlyValIleValValGlyIleValIleLeuIlePheThrGlyIleArgAspArgLysLys
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                                                                                                                                                                                                                                             AATAATCCAGGATTCCAAAACACTGATGATGTTCAGACCTCCTTT
                                                                                                                                                                                                                                                                                                AAAAATAAAGCAAGAAGTGGAGAAAATCCTTATGCCTCCATCGATATTAGCAAAGGAGAA
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Query Match:
                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the metalloenzyme Zace2, an angiotensin-CC converting enzyme is a zinc metalloenzyme Zace2, an angiotensin-CC converting enzyme is a zinc metalloenzyme zace2 can be expressed by standard crecombinant methodology. Zace2 polypeptides are useful for treating an inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), concludes a stargets for identifying modulators of zinc protease activity, for contract and as a basis for rational drug design for inhibitory contracts. The nucleic acids can be used to detect the expression of a corez gene in a biological sample, as probes for in vivo diagnosis and context and to detect a conditions, including left ventricular systolic dysfunction, progressive conditions, and treatment of atherosclerosis. Zace2 agonists may be used to treat infertility while Zace2 antagonists are used for inducing conference infertility. The present sequence represents a cDNA encoding the mouse case2.5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Angiotensin-converting enzyme, Zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases associated with inflammation such as arthritis and enterocolitis -
                                                                                                                                                                                                                                                                                                                                           Sequence 2638 BP; 802 A; 556
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27-AUG-1999;
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                                                                                                                       (ZYMO ) ZYMOGENETICS INC.
226 TATCAAAGTTCACTTGCTTCTTGGAATTATAATACTAACATTACTGAAGAAAATGCCCAA
                                                         166 ACCGAGGAAAATGCCAAGACATTTTTAAACAACTTTAATCAGGAAGCTGAAGACCTGTCT
                   41 TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
                                                                             21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
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99US-0384706.
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/product= "zace2-5"
/note= "the coding fragment is specifically claimed for"
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661
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420	1 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer	40	Qy
1365		130	Db
400	1 TyraspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe	38	Qy
1305		124	Db
380	1 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln	36	Qy
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360 1185	1 LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet	4 4	оу Оъ
340 1125	1 ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln	δ i	Qy
320	1 AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu	0	Qy
1065			Db
300 1005	1 LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln	8 4	Qy Db
280	1 CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer	26	Qу
945		88	Дъ
260 885	1 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly	24 82	Дy
240	21 GlnLeuileGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu	22	Qу
825		76	
220	11 AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly	20	Qy
765		70	dd
200	31 GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly	18	Qy
705		64	db
180	51 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr		Db
645			Qy
160	41 CysleuLeufeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu	14	Qy
585		52	Db
140	21 AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu	12	Qy
525		46	db
120	01 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu	10	Qy
465	:::	40	db
100	81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu	34	Qy
405			Db
80	61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla	28 6	Qy
345			Db

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TTCCTGTTCCGATCATCTGTTGCATATGCCATGAGAAAGTATTTTTCAATAATCAAAAAC
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                                                                                                                                                                                                                                                                                                                                                                 GAAGATGCCATCAGGATGTCTCGGGGCCGCATCAATGATGTCTTTGGCCTGAATGATAAC
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ATTGTCACTGGGATCAAAGGTCGAAAGAAGAAAAAATGAAACAAAAAGAGAAGAGAACCCCT
                                  ATATGGCTGATTATTTTTGGTGTTGTGATGGCACTGGTAGTGGTTGGCATCATCCTG
                                                                                                                                                                               IleTrpLeuIleValPheGlyValValMetGlyValIleValValGlyIleValIleLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiotensin-converting enzyme, Zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases associated with inflammation such as arthritis and enterocolitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2506 GCTCAGACTTCCTTT 2520
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27-AUG-1999;
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inactivator; ss.
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Qy 멍 Ş 밁 Qγ 밁 QΥ 밁 δÃ Вþ QΥ

Disclosure; Page 113-118; 125pp; English.

converting enzyme is a zinc metallopeptidase that plays roles in blood pressure regulation and fertility. Zace2 can be expressed by standard recombinant methodology. Zace2 polypeptides are useful for treating an inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), diseases associated with inflammation like arthritis and enterocolitis, as targets for identifying modulators of zinc protease activity, for screening or identifying new anglotensin-converting enzyme (ACE) inhibitors, and as a basis for rational drug design for inhibitory molecules. The nucleic acids can be used to detect the expression of a Zace2 gene in a biological sample, as probes for in vivo diagnosis and for detecting and localizing Zace2 gene expression in tissue samples, to detecting whether a subject's chromosomes contain a mutation in the Zace2 gene, and to detect aberrations associated with the Zace2 locus. Inhibitors of ACE are used for treating hypertension of various conditions, including left ventricular systolic dysfunction, progressi renal impairment, scleroderma renal crisis, congestive heart failure d to dysfunction, and treatment of atherosclerosis. Zace2 agonists may bused to treat infertility while Zace2 antagonists are used for inducin infertility. The present sequence represents a cDNA encoding the mouse invention relates to the metalloenzyme Zace2. protein Zace2, an angiotensin progressive

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        LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 300
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                                                                                                             GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240
                                                                                                                                                  GATTATTGGAGAGGGGACTATGAAGCAGAGGGAGCAGATGGCTACAACTATAACCGTAAC 765
                                                                                                                                                             GAAGAGTATGTGGTCCTGAAAAACGAGATGGCAAGAGCAAACAATTATAACGACTATGGG
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620 1965	AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal		ДЬ
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580 1845	GlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn		D Qy
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540 1725	TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis	6 0	Qy Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zace2; metalloenzyme; angiotensin-converting enzyme; ACE; fertility; zinc metallopeptidase; blood pressure; zinc protease; hypertension; ventricular systolic dysfunction; renal impairment; heart failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2506 GCTCAGACTTCCTTT
                                                                                                                                                 Angiotensin-converting enzyme, Zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or disease associated with inflammation such as arthritis and enterocolitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAY-2000; 2000WO-US11932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scleroderma renal crisis; atherosclerosis; antiinflammatory; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAR-2001 (first entry)
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27-AUG-1999;
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                                                                                               Disclosure; Page 103-104; 125pp; English.
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   invention relates to the metalloenzyme Zace2. verting enzyme is a zinc metallopeptidase that
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molecules. The nucleic acids can be used to detect the expression of a Zace2 gene in a biological sample, as probes for in vivo diagnosis and for detecting and localizing Zace2 gene expression in tissue samples, to determine whether a subject's chromosomes contain a mutation in the Zace2 gene, and to detect aberrations associated with the Zace2 locus. Inhibitors of ACE are used for treating hypertension of various conditions, including left ventricular systolic dysfunction, progressive renal impairment, scleroderma renal crisis, congestive heart failure due to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be used to treat infertility while Zace2 antagonists are used for inducing infertility. The present seminora represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pressure regulation and fertility. Zace2 can be expressed by standard recombinant methodology. Zace2 polypeptides are useful for treating an inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), diseases associated with inflammation like arthritis and enterocolitis, as targets for identifying modulators of zinc protease activity, for
                                                                                                                                                                                                                                                                                                                                                                                                                             screening or identifying new angiotensin-converting enzyme (ACE) inhibitors, and as a basis for rational drug design for inhibitory molecules. The nucleic acids can be used to detect the expression of
                                                                infertility. The participation in the participation of the human
                                                                The present sequence represents a degenerate sequence human zace2 protein.
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Sequence 2415 BP; 494 A; 218 C; 398 G; 335 Η, 970 other;

US-09-978-385-2 (1-805) x AAC84367 (1-2415)

Query Match:

Best Local Similarity:

Percent Similarity:

0 3509.00 80.00% 80.00% 81.78%

Length: Matches: Conservative:

Indels: Gaps: Mismatches: Alignment Scores:

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Qy Вb 밁 δÃ ρy Š 밁 Q В γg DЪ Qy 밁 δÃ 밁 δõ 밁 Ω В 361 301 121 61 1 MetSerSerSerSrTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr TAYCARWSNWSNYTNGCNWSNTGGAAYTAYAAYACNAAYATHACNGARGARAAYGTNCAR ATHGARGARCARGCNAARACNTTYYTNGAYAARTTYAAYCAYGARGCNGARGAYYTNTTY 120 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe ATGWSNWSNWSNTGGYTNYTNYTNWSNYTNGTNGCNGTNACNGCNGCNCARWSNACN AAYACNATGWSNACNATHTAYWSNACNGGNAARGTNTGYAAYCCNGAYAAYCCNCARGAR CARCARAAYGGNWSNWSNGTNYTNWSNGARGAYAARWSNAARMGNYTNAAYACNATHYTN AAYATGAAYAAYGCNGGNGAYAARTGGWSNGCNTTYYTNAARGARCARWSNACNYTNGCN GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly MGNYTNTGGGCNTGGGARWSNTGGMGNWSNGARGTNGGNAARCARYTNMGNCCNYTNTAY ${\tt ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr}$ TGYYTNYTNYTNGARCCNGGNYTNAAYGARATHATGGCNAAYWSNYTNGAYTAYAAYGAR CysLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 180 480 360 300 100 80 180 60 40

converting enzyme

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AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly

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                26-MAR-1999;
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                                                                                                             Homo sapiens
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CC of a polyuncilectide agent that modulates the expression of the nucleic caid or its complement (i.e. gene therapy). The nucleic acid can be used to identify an agent that modulates the expression or activity of the cultic acid can be used to isolate the protein. The nucleic acid can be used in diagnostic assays for determining nucleic acid expression can be used in diagnostic assays for determining nucleic acid expression can see used in diagnostic assays for determining nucleic acid expression cas well as activity in the context of a biological sample (e.g., blood, configuration). The nucleic acid expression can see the context of a biological sample (e.g., blood, configuration) to determine whether an individual has a disease or configuration. The nucleic acid can be used to detect mutations in protease genes and gene can be used to detect mutations in protease genes and gene configuration probes to detect naturally-occurring genetic mutations in caprotease gene. The nucleic acid can be used as protease mediated disorders e.g., proliferative, developmental or haematopoietic disorders. The nucleic acid can be used as probes, primers, in biological assays, to determine patterns of gene expression, to design ribozymes and to construct transgenic animals. The present sequence represents one of the 268 cated human G-rotesion-confied rotease entrence.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising a nucleotide sequence of 546 base pairs, one of 268 fully defined in the specification. Also disclosed are production of an isolated polypeptide encoded by the nucleic acid, comprising introducing the nucleic acid into a host cell and culturing under conditions to express the protein from the nucleic acid, use of an antibody to detect the encoded protein in a sample and to modulate its in vivo activity, identifying agents that bind to the protein and identification activity, identifying agents that bind to the protein and identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides encoding protease homologs of the G-protein-coupled protease family, useful in identifying agonists and antagonists for diagnosis and treatment of protease mediated disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-129545/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated human protease nucleic acid molecule
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CCAAAACATGAATAATGCTGGGGACAAAATGGTCGTGCCTTTTTAAAGGAACAGTCCACA
                                                                                                                                                                                                                                                                            CATTGAGGAACAGGCCAAGACATTTTTTGGACAAGTTTAACCACGAAAGCCGAAGACCTG
                                                                                                       PheTyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThr-AsnIleThrGluGluAsnVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGCCAATGGTGGACCAGGCCTGGGATGCACCAGAGAATATTCAAGGAGGCCCGAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATGAACATCTTCATGCCTATGTGAGGGCAAAGTTGATGAATGCCTATCCTATATC
                                                                                                      laAlaThrPro-LysHisLeuLysSerIleGlyLeuLeu---SerProAspPheGlnGlu 430
                                                                                                                                                                           euArgAsnGlyAlaAsnGluGlyPheHisGluAlaValGlyGluIleMetSerLeuSerA 412
                                                                                                                                                                                                                  CTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGCTGCACAACCTTTTCTGG 1106
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  Antiarteriosclerotic; hepatotropic;
              Human; molecules for disease detection and treatment;
                                        Human cDNA encoding an mddt protein, clone LI:347572.1:2000MAY01.
                                                                                                                           AAS42515
                                                                      18-DEC-2001
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                                                                                                                                                                                                                                                                                    TGGTCACTGCCCCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGAGTACCGACTGGAGTCCATATGCAGACCAAAAGCATCAAAGTGAGGATAAAGCCTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGGAACATGAATGTAAGGCCACTGCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrLeuAlaLeuGluAsnValValGlyAlaLys-AsnMetAsnValArgProLeuLeuAs 586
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24-FEB-2000;
16-MAY-2000;
17-MAY-2000;
17-MAY-2000;
17-MAY-2000;
17-MAY-2000;
17-MAY-2000;
                                                                                                                                                                        New disease detection and treatment molecule polynucleotides and polypeptides, useful for diagnosis and treatment of arteriosclerosis, cirrhosis, psoriasis, cancer, autoimmune disorders, diabetes mellitus, asthma and multiple sclerosis
                                                                                                                                                                                                                                                                               Liu TF, Ro
Wright RJ,
                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressive; antidiabetic; antiasthmatic; neuroprotective; osteopathic; antiarthritic; cell proliferative disorder; arteriosclerosis; cirrhosis; psordissis; cancer; adenocarcinoma; leukaemia; breast cancer; autoimmune disorder; AIDS; acquired immunodeficiency syndrome; Addison's disease; diabetes mellitus; asthma; multiple sclerosis; osteoarthritis.
                                                                                                                                                  Claim 1; Page 139-140; 183pp; English.
                                                                                                                                                                                                                                   P-PSDB;
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E, Flores V, Fong WT,
Roseberry AM, Rosen B
J, Yap PE, Yu JY, Br
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2000US-0205285.
2000US-0205286.
2000US-0205287.
2000US-0205323.
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                                                                                                                                                                                                                                                                 ille SC, Shah P, Chalup MS, Char
, Dahl CR, Dam TC, Daniels SE;
WT, Greenawalt LB, Hillman JL,
en BH, Russo FD, Stockdreher TK,
Bradley DL, Bratcher SR, Chen W
                                                                                                                                                                                                                                                                               Chen W;
                                                                                                                                                                                                                                                                                                                           Chang
                                                                                                                                                                                                                                                                                                      Jones
                                                                                                                                                                                                                                                                                          Datto
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The invention relates to novel human molecules for disease detection and treatment (mddt proteins) and the polynucleotides encoding them. The MIDT polynucleotides and polypeptides are useful for diagnostic and therapeutic purposes e.g. to diagnose and treat cell proliferative disorders (e.g. arteriosclerosis, cirrhosis and psoriasis) cancers (e.g. adenocarcinoma, leukaemia and breast cancer) autoimmune disorders (e.g. acquired immunodeficiency syndrome (AIDS) and Addison's disease) diabetes mellitus, asthma, multiple sclerosis, osteoarthritis, and many more diseases given in the specification. The present sequence encodes an mddt protein of the invention.

3474 BP; 1019 A, 696 ç, 781 ç, 978 Τ; 0 other;

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                                                             Best Local Similarity: Query Match:
DB:
                                                 US-09-978-385-2
                                                                               Percent Similarity:
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(1-805)
                                                            7.79e-294
3119.00
85.94%
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                                                 (1-3474)
                                                                              Length:
Matches:
Conservative:
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Indels:
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730
22
51
72
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338 nValGlnLysAlaValCysHis-ProTh
319 lyLeuProAsnMetThrGlnGlyPheTrp-GluAsnSerMetLeu-Thr
99 pGlnAlaTrpAspAlaGlnArgIlePheLysGluAla-GluLysPheP
279 rSerLeuThrValProPheGlyGlnLysProAsnIleAspValThrAspA
260 GlyCysLeuProAlaHisLeuLeuGlyAspMetTrp-GlyArgPheTr
240 LeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyr
220 yGlnLeuIleGluAspValGluHisThr-PheGluGluIleLysProLeuTyr
201 pTyrTrpargGlyaspTyrGluValAsnGlyValAspGlyTyrAspTyrS
182 luTyrValValLeuLysAsnGluMetAlaArgAlaAsnHis
y 162 euTrpAlaTrpGluSerTrpArgSerGluValGlyLy
142 euLeuLeuGluProGlyLeuAsnGluIleMetAle
124SerThrIleTyrSerThrGlyLy. ::: 453 AGCCACCAATCCTAACAGTAACTGGAAA
107 lLeuSerGluAspLysSerLys
35 uGlnLeuGlnAlaLeuGlnGlnAsnGlySe :::
76 GlnSerThrLeuAlaGln-MetTyrProL
alGln-AsnMetAsnAsnAlaGlyA: CCAACAACATGCAATAAGTTGCTGGCG
40 PheTyrGlnSerSer-LeuAlaSer-Tr)

746	726 lylleGlnProThrLeuGlyProProAsnGlnProProValSerIleTrpLeuIleValP	Qy
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2252	93 CITTATATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	
706	aProLysAsnValSer-AspIleIleProArg-ThrGluValGluLysAlaIle	Qy
687 2192	667 luGluAspValArgValAlaAsnLeuLysProArgIleSerPheAsnPhePheValThrA 	Оу
667 2132	648 aTyrAlaMetArgGlnTyrPheLeu-LysValLysAsnGlnMetIleLeuPheGlyG 	Db Qy
648	629 y-AspLysalaTyrGluTrpAsnAsp-AsnGluMetTyrLeuPheArgSerSer-ValAl	Qу
2072		ДЪ :
0 0	10 TrpSerProTyrAlaAspGlnSerIle-LysValArgIleSerLeuLysSerAlaLeuG 	Qy Db :
609	590 ProLeuPheThrTrpLeuLysAspGlnAsnLysAsnSerPheValGlyTrpSerThrAsp	Qy
1952		Db :
589	570 uGluAsnValVal-GlyAlaLysAsnMetAsnValArgPro-LeuLeuAsnTyrPheGlu	Qγ
1892		Db :
570	551 lyGlnLys-LeuPheAsnMetLeuArgLeuGlyLys-SerGluProTrpThrLeuAlaLe	Qy
1832		Db 1
551	533 AlaLysHisGluGlyProLeuHisLys-CysAspIle-SerAsnSerThrGluAlaG	Qy
1772		Db 1
532	514 ArgTyrTyrThrArgThrLeu-TyrGlnPheGlnPheGln-GluAlaLeu-CysGlnAla	Qy
1712		Db :
513 1652	494 spGluThrTyr-CysAspProAlaSerLeuPheHisValSerAsnAspTyrSerPheile 	Qy
494	475 ysLys-TrpTrpGluMetLysArgGlu-IleValGlyVal-ValGluProValProHisA	Qy
1592		Db 1
475	455 tLeuGluLysTrpArgTrpMetValPheLys-GlyGluIleProLysAspGlnTrpMetL	Qy
1532		Db 1
455	435 uIleAsnPheLeuLeuLysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMe	Qy
1472		Db 1
435 1412	416 sHisLeuLysSerIleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGl	Qy Db 1
416	397 -AsnGluGlyPheHisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLy	Qy
1352		Db 1
1292		Db 1

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RESULT 16
AAC84 369
ID AAC84
XX AC84
XX AC84
XX AC84
XX Zace2
KW Zace2
KW Zace2
KW Zace2
KW Ventr
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             converting enzyme is a zinc metallopeptidase that plays roles in blood pressure regulation and fertility. Zace2 can be expressed by standard recombinant methodology. Zace2 polypeptides are useful for treating an inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis), diseases associated with inflammation like arthritis and enterocolitis, as targets for identifying modulators of zinc protease activity, for screening or identifying new angiotensin-converting enzyme (ACE) inhibitors, and as a basis for rational drug design for inhibitory molecules. The nucleic acids can be used to detect the expression of a Zace2 gene in a biological sample, as probes for in vivo diagnosis and for detecting and localizing Zace2 gene expression in tissue samples, to detect and to detect abstraction sassociated with the Zace2 locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 112-113; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiotensin-converting enzyme, Zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases associated with inflammation such as arthritis and enterocolitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piddington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    zinc metallopeptidase; blood pressure; zinc protease; hypertension; ventricular systolic dysfunction; renal impairment; heart failure; scleroderma renal crisis; atherosclerosis; antiinflammatory; mouse; antiarthritic; bradykinin inactivator; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zace2; metalloenzyme; angiotensin-converting enzyme;
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conditions, including left ventricular systolic dysfunction, progressive renal impairment, scleroderma renal crisis, congestive heart failure due to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be used to treat infertility while Zace2 antagonists are used for inducing
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                                   HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly
                                                                                           GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu
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CAYGCNTAYGTNMGNMGNAARYTNATGGAYACNTAYCCNWSNTAYATHWSNCCNACNGGN
                                                                      CARYTNATHGARGAYGTNGARMGNACNTTYGCNGARATHAARCCNYTNTAYGARCAYYTN
                                                                                                                                          GAYTAYTGGMGNGGNGAYTAYGARGCNGARGGNGCNGAYGGNTAYAAYTAYAAYMGNAAY
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                                                                              AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal
                                                                                                                                                      ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys
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                                                                                                                                                                                   Peptide
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                                             (INRM ) INST
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                                                                                                                                                                                                                                                                              sterility;
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                        Alhenc-Gelas F,
                                               NAT SANTE RECH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A bank of human testicular cDNA in Lambda gtll was screened with a probe containing the final 3248 nucleotides of endothelial ACE. The complete sequence of tACE was reconstructed from 4 separate clones. It encodes a 711 amino acid mature protein and a 21 residue signal peptide. The 228-2224 sequence is identical to the 1944-9940 region of endothelial ACE. The isolated nucleic acid sequence is inserted into a plasmid for expression of polypeptides. The invention also covers parts of the sequence comprising all or part of the 29-229 sequence, any sequence differing from tACE only by silent substitutions and nucleic acids which hybridise to tACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2477 BP; 536 A; 811 C; 695 G; 435 T; 0 other;
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                              TrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGlyGlnLeu 222
                                                                                                                                                                                                                  CAGCTCGAGCCAGATCTGACGAATGTGATGGCCACATCCCGGAAATATGAAGACCTGTTA
                                                                                                                                                                                                                                                  LeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGluArgLeu
                                                                                                   TyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTyr 202
                                                                                                                                                                        TrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyrGluGlu
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   TGGAGGTCTATGTACGAGACACCATCCCTGGAG---
                                                                      TACGTGGAACTCATCAACCAGGCTGCCCGGCTCAATGGCTATGTAGATGCAGGGGACTCG
                                                                                                                                             TGGGCATGGGAGGGCTGGCGAGACAAGGCGGGGAGAGCCATCCTCCAGTTTTACCCGAAA
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                                                                                                                                                                                                                                                                                                                     MetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGluCysLeu 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTGATGTGAACCAGTTGCAGAACACCACTATCAAGCGGATCATAAAGAAGGTTCAGGAC
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                                                                                                                                                                                                                                                                                                                                              receptors 1 and 2. The method comprises determining the sequence at one or more polymorphic positions within these genes, and comparing the pattern of polymorphisms from the individual with a reference polymorphic pattern obtained from a population of individuals exhibiting a predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to cardiovascular disorders such as myocardial infarction, unstable angina, hypertension, atherosclerosis and stroke. They are also useful for predicting the likely cardiovascular status of a pattent given a treatment regimen comprising administration of cardiovascular drugs (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-blockers) or calcium channel blockers). One or more polymorphic markers provides a basis for predicting the outcome of a treatment regimen.
Fragments of the genes comprising a polymorphic site may be used as primers and probes for detecting genetic polymorphisms or in molecular library arrays for high throughput screening. The genes, and the proteins they encode are useful in the screening of potential cardiovascular drugs. Determination of an individual's polymorphic pattern reduces or eliminates trial and error in selecting a treatment for a particular individual cardiovascular patient. It also provides the ability to eliminate patients from clinical trials who are predicted to be non-responsive, or at a risk for an adverse response, to a particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes encoding angiotensin-converting enzyme (ACE), angiotensin II receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin, aldosterone synthase, endothelin receptor type A and beta-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Angiotensin-converting enzyme gene; ACE; coding region; polymorphism; polymorphic marker; cardiovascular disease; myocardial infarction; unstable angina; hypertension; atherosclerosis; stroke; prognosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotides 1451-1783 in intron 16.
                                                                                                                                                                                                                                      2402 GCGGGGAGAGCCATCCTCCAGTTTTACCCGAAATACGTGGAACTCATCAACCAGGCTGCC
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                                                                                                                                                                                                                                                                                                                                         ThrValLysLeuGlnLeuGlnAlaLeuGlnGlnAsnGlySerSerValLeuSerGluAsp 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----CTGAAGTACGGCACCCAGGCCAGGAAGTTTGATGTGAACCAGTTGCAGAACACC
GluIleLysProLeuTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAla
                                                                                                                 ValAspGlyTyrAspTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGlu 231
                                                                                                                                                                                                                                                                                                                                                                                                 GTGTGCCACCCGAATGGC-----AGCTGCCTGCAGCTCGAGCCAGATCTGACGAATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt PheLeuLysGluGlnSerThrLeuAlaGlnMetTyrProLeuGlnGluIleGlnAsnLeu}
                                                                                                                                                          CGGCTCAATGGCTATGTAGATGCAGGGGACTCGTGGAGGTCTATGTACGAGACACCATCC
                                                                                                                                                                                               ArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrpArgGlyAspTyrGluValAsnGly 211
                                                                                                                                                                                                                                                                         ValGlyLysGlnLeuArgProLeuTyrGluGluTyrValValLeuLysAsnGluMetAla
                                                                                                                                                                                                                                                                                                                    ATGGCCACATCCCGGAAATATGAAGACCTGTTATGGGCATGGGAGGGCTGGCGAGACAAG
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CCGCTGCTGGACTGGCTCCGCACGGAGAACGAGCTGCATGGGGAGAAGCTGGGCTGGCCG
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                                                                                                                                                                                                                                                                                             Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta; amyloid precursor protein; tissue-specific expression control; human AP pathway modulator; gene therapy; gene; ds.
                                                                                                                                                                                                                                      WO200226820-A2.
                                                                                                                                                                                                                                                                                                                        DNA of
                                                                                                                                                                                                                                                                                                                                   27-JUN-2002
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                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                 /note= "No start codon"
                                                                                                                                                                                                                                                      /product= "Protein of human homologue hCP51674"
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Cohen D, Dengler UJ, Reinhardt MWHM, Zusm SAON) 14-JUN-2001; 01-OCT-2001; 2001WO-EP11345 29-SEP-2000;) NOVARTIS AG.
) NOVARTIS-ERFINDUNGEN VERW GES MBH 2000US-236893P 2001US-298309P Finelli AL,

New transgenic fly, containing DNA encoding an Abeta portion of human APP, useful for identifying agents which modulate the APP pathway and which can be used to treat Alzheimer's disease -

2002-315796/35

Zusman

Freuler F,

Example 4; Page 93-94; 129pp; English.

The invention relates to a transgenic fly whose genome comprises DNA encoding a polypeptide having the Abeta portion of human amyloid precursor protein (APP), fused to a signal sequence. The DNA sequence encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in the specification. The DNA sequence is operably linked to a tissue-specific expression control sequence. Expression of the sequence gives the fly an altered phenotype. The purpose of the invention is for identifying agents that inhibit or promote the expression and/or function of genes or encoded polypeptides which modify the APP pathway. The agent that a compound, triple helix DNA, antisense oligonucleotide, double stranded by the approach of the sequence of the inventor of the sequence of the inventor of the sequence of the sequence of the sequence of genes or encoded polypeptides which modify the APP pathway. The agent that a compound, triple helix DNA, antisense oligonucleotide, double the sequence of stranded RNA molecule, ribozyme, or particularly an antibody. It is used to treat conditions such as Alzheimer's disease. The agent can be used as an APP pathway modulator or in gene therapy. This polynucleotide sequence DNA of the APP related human homologue hCP51674.

Sequence 4022 ВP; 856 A; 1262 C; 1174 G; 728 T; 2 other;

Query Match: DB: Best Local Similarity: Alignment Percent Similarity: Pred. No : : Scores: 7.74e-120 1337.00 61.05% 41.73% 31.16% Conservative: Mismatches: Indels: Matches: Length: 4022 255 118 204 34

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SerThrAspTrpSerProTyrAlaAspGlnSer

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LeuGlyLysGly---AspPheArgIleLeuMetCysThrLysValThrMetAspAspPhe
                                                                                      SerMetLeuThrAspProGlyAsnValGlnLysAlaValCysHisProThrAlaTrpAsp
                                                                                                                                                  GCTGATGATTTCTTCACCTCCCTGGGGGCTGCTGCCGTGCCTCCTGAGTTCTGGAACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4024 BP; 857 A; 1263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAR04111.
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                                                                                                     MetAlaAsnSerLeuAspTyrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu
                                                                                                                                                                                       GTGTGCCACCCGAATGGC-----AGCTGCCTGCAGCTCGAGCCAGATCTGACGAATGTG
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                                                                    ATGGCCACATCCCGGAAATATGAAGACCTGTTATGGGCATGGGAGGGCTGGCGAGACAAG
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Command line parameters:

-WODEL-frame+_p2n.model -DEV=xlp
-O-cgn2_1/USPT0_spool/US09978385/runat_28022003_104716_1351/app_query.fasta_1.967
-DB-EST -OFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -HIR_MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINIEN=2000000000
-USER=US09978385_@CGN_1_1_2874_@runat_28022003_104716_1351 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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ALIGNMENTS

AUTHORS TITLE	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BC032938	RESILT 1
Strausberg, R. Direct Submission	<pre>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 337)</pre>	Homo sapiens	human.	HTC.	BC032938.1 GI:21432080	BC032938	A) 2, clone IMAGE:4830668, mRNA.	rting enz	BC032938 3337 bp mRNA linear HTC 17-JUN-2002		

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              AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140
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AATACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAA
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov Series: IRAK Plate: 34 Row: i Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11225608
This clone has the following problem: frame shifted.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
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                                                                                                                            GTTCAGACCTCCTTT 2453
                                                                                                                                                  ValGlnThrSerPhe 805
                                                                                                                                                                      ATCTTCACTGGGATCAGAGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAGAAAATCCT 2378
                                                                                                                                                                                                                                                                             ATATGGCTGATTGTTTTTGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTG 2318
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                                                                                                                                                                                                                                                                                                                                                 SerLeuGluPheLeuGlyIleGlnProThrLeuGlyProProAsnGlnProProValSer 740
                                                                                                                                                                                                                                                                                                                                                                                    GAAAAGGCCATCAGGATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLySProArgIleSer 680
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                                    prime, mRNA sequence.
AL551235
                     AL551235.1 GI:12888986
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US-09-978-385-2 (1-805) x AL551235 (1-987)
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423 GAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCACTGCA
                           668 GluAspValArgValAlaAsnLeuLysProArgIleSerPheAsnPhePheValThrAla 687
                                                                                                                            648 AlaTyralaMetArgGlnTyrPheLeuLysValLysAsnGlnMetIleLeuPheGlyGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         568 LeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsnValArgProLeuLeuAsnTyr
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                                                                                                    GCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGGGGAG
                                                                                                                                                                                                  CTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATCTGTT
                                                                                                                                                                                                                                             LeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLeupheArgSerSerVal 647
                                                                                                                                                                                                                                                                                                      ACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr.
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1 (bases 1 to 987)
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182 c 211 g 270 t
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Alzawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yananaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
                                                                                                                                                                                                                             Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Sakaguencing pipaline with 384 multicapillary sequencer sequencem pipaline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
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/db_xref="MGD:MGI:1902242"
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/clone_lib="RIKEN_full-length enriched mouse cDNA library"
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KNOTVPFLEEDVRVSDLKPRVSFYFFVTSPQNVSDVIPRSEVEDAIRMSRGRINDVFG
LNDNSLEFLGIHFTLEPPYQPFVTIWLIIFGVVMALVVVGIIILIVTGIKGRKKKNET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB25723.1"
/protein_id="BAB25723.1"
/db_xref="Gi:12842767"
/db_xref="MGD:MG:1917258"
/db_xref="MGD:MG:1917258"
/tanslation="MLSLGNSEPWTKALENVVGARNMDVKBLLNYFQPLFDWLKEQNR/
/translation="MLSLGNSEPWTKALENVVGARNMDVKBLLNYFQPLFDWLKEQNR/
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/note="putative"
                                                                                                                                                                                                                                    KREENSYDSMDIGKGESNAGFQNSDDAQTSF"
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Tissue Procurement: Life Technologies, Inc.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLCM1335 row: d column:
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                                                                                                                                                                                                                                                                        quality sequence stop: 619.
/clone_lib="NIH_WGC_75"
/clone_lib="NIH_WGC_75"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
sfiI (gycogoctgygcc); Site_2: sfiI (gycoattatgycc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGGCGGCGACATG-dT(30)BN-3' (where B = A,
C, Or G and N = A, C, G, Or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
                                                                                                                                                                          /clone="IMAGE:4594140"
                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                Location/Qualifiers
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US-09-978-385-2 (1-805) x BG401683 (1-879)
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663 GGCATATTGCTATTACGGAGTACTTTTTAAAGTAAACATCG-----ATGATCTTTGGGG
                         647 lAlaTyr-AlaMetArgGlnTyrPheLeuLysValLysAsnGlnMetIleLeuPheGlyG
                                                                                                  610 T---GGAGATAAGCA-TATGACTGGACG---ACATGAATTGTCCTGTNCCGATCATCTGT
                                                                                                                                                    627 aLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSerSerVa
                                                                                                                                                                                                                                                                                                                    490 TTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTCTTTTGTGGGATGGACT
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ThrTyrCysAspProAlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyr 515
                                                                                          AAGTGGTGGGAGATGAAGCCGGAGATCGTTGGTGGTGGAGCCTCTGCCTCATGATGAA
                                                                                                                          TTAGAGAAGTGGAGGTGGATGGTCTTTCGGGGTGAAATTCCCCAAAGAGCAGTGGATGAAA
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 766)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.2 kb and
                                                                                                         /clone="IMAGE:5296531"
/clone_lib="NIH_MGC_97"
                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                        /lab_host="DH10B"
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TOShiyuki and Piero Carninci (RIKEN)
TOSHA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
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/clone_lib="NIH_MGC_97"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs=r@mail.nih.gov
Tlssue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11752 row: j column: 05
High quality sequence stop: 606.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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1 (bases 1 to 609)
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603255121F1 NIH_MGC_97 Homo sapiens
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/clone="IMAGE:5297380"
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                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian
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/clone="IMAGE:4223312"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B_(T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPOI
                                                                         /db_xref="taxon:10090"
                                                                                              /strain="FVB/N"
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                                                                                                       TCATGCCTATGTGAGG
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                                                                                                                                                                          ACAGTGATTGAGA---TGTGAACGTACTTCGCAGAAA---TCAGCATTGGGTGAGCCTCT
                                                                                                                                                                                                           yGlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLe 240
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AA162058 55 bp mRNA linear EST 12-FEB-199 ms31h11.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:608613 5' similar to SW:ACE_MOUSE P09470
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                                    LeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrpArgGly
                                                                                                                                                                                                                                                                                                                     ProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGluArgLeuTrpAlaTrp
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CTGAAAAACGAGATGGCAAGAGCAAACAATTATAACGACTATGGGGATTATTGGAGAGGG
                                                                                                                                  GAGGGCTGGAGGCTGAGGTTGGCAAGCAGCTGAGGCCGTTGTATGAAGAGTATGTGGTC
                                                                                                                                                                       High quality sequence stop: 446.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of MedicineP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia;
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                                                                                                                                                                                                                                                                                                         Email: genome res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carnincl.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 686)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishi, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., D., Shibata, K., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y., PYYEN Mouroe ceme, Aracham, M., Tanaka, T., Takanashi, F., Takeda, Y., Tanaka, T., Toya, T., PYYEN Mouroe ceme, Aracham, M., Tanaka, T., Toya, T., PYYEN Mouroe ceme, Aracham, M., Tanaka, T., Takanashi, Y., PYYEN Mouroe ceme, Aracham, M., Tanaka, T., Toya, T., PYYEN Mouroe ceme, Aracham, M., Tanaka, T., Toya, T., PYYEN Mouroe ceme, Aracham, M., Tanaka, T., Toya, T., PYYEN Mouroe ceme, Aracham, M., Tanaka, T., Toya, T., PYYEN Mouroe ceme, Aracham, M., Tanaka, T., Toya, T., PYYEN Mouroe ceme, Aracham, M., Tanaka, T., Toya, T., PYYEN Mouroe ceme, Aracham, M., Tanaka, T., Toya, T., PYYEN Mouroe ceme, Aracham, M., Tanaka, T., Toya, T., PYYEN Mouroe ceme, Aracham, M., Tanaka, T., Tanaka, T., Pyyen M., Pyy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                     Hayashizaki,Y
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                                                                                                                            ,Y. and Hayashizaki,Y.
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                                                                                                                                Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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121 ASnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu 140
                                                                                                                                                                 101 GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu 120
                                                                                                                                                                                                                                                272 CAAAGTTTCTCACTACAAGAAATCCAGACTCCGATCATCAAGCGTCAACTACAGGCCCTT
                                                                                                                                                                                                                                                                                                                                                                     212 AAGATGAGTGAGGCTGCAGCCAAATGGTCTGCCTTTTATGAAGAACAGTCTAAGACTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 TATCAAAGTTCACTTGCTTCTTGGAATTATAATACTAACATTACTGAAGAAAATGCCCAA
                                                                                                                                                                                                                                                                               81 GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                    61 AsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
                                                                                                                        CAGCAAAGTGGGTCTTCAGCACTCTCAGCAGACAAGAACAACAGTTGAACACAATTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTCCAGCTCCTGGCTCCTTCTCAGCCTTGTTGCTGTTACTACTGCTCAGTCCCTC
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Mapping of 1932 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, L72-L86 (2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcriptase and subsequently enriched for full-length by cap-trapper. Second strand CDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAGTTAATTAAATTAATCCCCCCCCCCCC 3']"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepared by using trehalose thermo-activated reverse
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/dev_stage="adult"
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/clone="C630041D11"
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/strain="C57BL/6J"
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US-09-978-385-2 (1-805) x BG428060 (1-452)
                                                                                             Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 452)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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602501471F1 NIH_MGC_75 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: LLCM1367 row: n column: 18 High quality sequence stop: 450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Plate: LLCM1367 row:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
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/db_xref="taxno:9066"
/clone="IMAGE:4615121"
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/lab host="0H10B (T1 phage-resistant)"
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BM030353
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                                                                                                                                                                                                                                           USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                          Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
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                                                                                                                                                                    Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                    Contact: Smith TPL
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                                                                     Plate: 120 row: B column: 16 Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                              BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                              FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                  PCR PRimers
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/organism="Bos taurus"
/db_xref="taxon:9913"
                                                     Location/Qualifiers
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RESULT 15
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                                                                                                                                                                                                                                                     ACCTACCCTTCCTATATC 556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAAGAGCCAACAATTATGAGGACTACGGGGACTATTGGAGAGGGGGATTATGAGGTGACT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGTTGGCAAGCAACTAAGGCCATTGTATGAAGAGTATGTGGTCCTAGAAAATGAGATG
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1 (bases 1 to 741)
                                                          Homo sapiens
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                                                                                                                                  mRNA sequence.
BG772384
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602722306F1 NIH_MGC_97 Homo
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/lab_host="DH10B"
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138 roGlnGluCysLeuLeuGluProGlyLeuAsnGlu-IleMetAlaAsnSerLeuAsp 157
                                    418 TTCTCAAATACACATGAGCACCATCTACAGTACTGGAACCAGTCTGTAACCCAGATAATC
                                                                                                        358 TCAGCACAACACTGGGTCTTCAGTGCTCTCAGAAGACAAGAGCAACACGGTTGAACACAA 417
                                                                                                                          100 uGlnGlnAsn---GlySerSerValLeuSerGluAspLysSerLys-ArgLeuAsnThrI 119
                                                                                                                                                                          298 CAATATGTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCT
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                                                                                                                                                                                                                                                                                                                 61 ASnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAla
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                                                        leLeu-AsnThr-MetSerThrIleTyrSerThrGly-LysValCysAsnProAspAsnP 138
                                                                                                                                                                                                                                                                                                                                                                                                     | IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe | 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGTTGCTGTAACTGCTGCTCAGTCCACC 117
                                                                                                                                                                                                                                                 AACATGAATAATGCTGGGGACAAATGGTCTGCCTTTATAACGGAACAGTCCACACTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: LLAM10774 row: k column: 02
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/db_xref="taxon:9606"
/clone="IMAGE:4839289"
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                                                  250 AsnAlaTyr---ProSerTyrIleSerProIleGlyCysLeuProAlaHisLeuLeuGly 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11417 row: j column: 20
High quality sequence stop: 797.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-*organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber full-length clones and clones and
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Invitrogen). Research Genetics tracking code 013.
this is a NIH_MGC Library."
a 244 c 230 g 157 t
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/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:5167987"
/clone_lib="NIH_MGC_119"
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408 MetSerLeuSerAlaAlaThrProLysHisLeuLysSerTleGlyLeuLeuSerProAsp 427
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                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Aaron Hsueh
                                                                                                                                                                                                                     1 (bases 1 to 1154)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Agencourt Bioscience Corporation
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                 382 GTTGTGATGGCACTGGTAGTGGTTGGCATCATCCTGATTGTCACTGGGATCAAAGGT 441
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BI415293 900 bp mRNA linear EST 14-AUG-2001 6029872899F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5143199 5', mRNA sequence.
BI415293
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High quality sequence stop: 756.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov Plate: LLAM12145 row: d column: 24
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/clone="IMAGB:5504231"
/clone=lib="NCI_CGAP_Ov44"
/clone=lib="NCI_CGAP_Ov44"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: ovary, PMSG-treated; Vector:
pCMV-SPORT6.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
232 c 266 g 334 t 2 others
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Plate: LLAM11353 row: a column: 24
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Tissue Procurement: Gilbert Smith,
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National Institutes of Health, Mammalian Gene Collection (MGC)
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National Institutes of Health, Mammalian
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Tissue Procurement: Life Technologies,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/clone_lib="NIH_MGC_119
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Plate: LLAM11429 row: c column: 16
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1 (Dases 1 to 778)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5172423"
/clone_ib="NHH_MGC_119"
/tissue_type="medulia"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for each of the control of the 
                                                                                                                                                                                                                                                                                                       full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

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Search completed: March 7, 2003, 09:47:36 Job time: 2390 secs

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US-08-280-116-40
US-08-481-626-1
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US-09-162-484-1
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ALIGNMENTS

RESULT 1

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Patent No. 6194556
                              TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL
                                            REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-7000
TELEFAX: 617-832-7000
                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold E. Beth
              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Acton, Susan L.
APPLICANT: Robinson, Keith E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
NUMBER OF SEQUENCES: 14
LENGTH:
                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 11-DE
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: AFFICIAL E., Beth
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIA-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08989299
Patent No. 6194556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Acton, Susan L.
APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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ADDRESSEE: FOLEY, HC
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CITY: Boston
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Best Local Similarity:
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Query Match:
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                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                              Score:
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2350
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION:
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PheTyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThr-AsnIleThrGluGluAsnVa
                                            rIleGluGluGlnAlaLysThr-PheLeuAspLysPheAsnHisGlu-AlaGluAspLeu
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3291.0
92.62%
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Matches:
Conservative:
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TOPOLOGY: 11;
MOLECULE TYPE:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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APPLICANT: Alhenc-Gelas, Francois
APPLICANT: Hubert, Christine
APPLICANT: Corvol, Pierre
APPLICANT: Coverier Constant Cod
TITLE OF INVENTION: Uses, Especially
TITLE OF INVENTION: Enzyme in the Or
                                         В
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APPLICATION NUMBER: US/08/481,626
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/656,183
FILING DATE: 04-MAR-1991
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FR 89-09062 FILING DATE: 05-UUL-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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ZIP: 20005-3315
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ADDRESSEE: Dunner
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                                                                                                                                                                                                 209 ACATCAGCCCAGAGCCCAAACCTGGTGACTGATGAGGCTGAGGCCAGCAAGTTTGTGGAG 268
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                                         269 GAATATGACCGGACATCCCAGGTGGTGGGAACGAGTATGCCGAGGCCAACTGGAACTAC 328
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                                                                              31 LyspheAsnHisGluAlaGluAspLeuPheTyrGlnSerSerLeuAlaSerTrpAsnTyr 50
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63 AsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAlaGlnMet 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Testicular Angiotensin Converting Enzyme (ACE) and in
Uses, Especially for the In Vitro Screening for this
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12	MetGlyH1S11eG	Qy Db
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8 0	LeuGlnLeuGlnAlaLeuGlnGln 1 ::::: ::: CGGATCATAAAGAAGGTTCAGGAC 4	Qy
24	::: 389 AACCACACC	Db

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US-09-050-159-130

; Sequence 130, Application US/09050159A
; Patent No. 6197505
; GEMERAL INFORMATION:

; APPLICANT: No. 6197505berg, Leif T
; APPLICANT: Andersson, Maria K
; APPLICANT: Linstrom, Per H
; TITLE OF INVENTION: METHODS FOR ASSESSING CARDIOVASCULAR STATILE OF INVENTION: COMPOSITIONS FOR USE THEREOF
; FILE REFERENCE: 1248/10042
; CURRENT APPLICATION NUMBER: US/09/050,159A
; CURRENT FILING DATE: 1998-03-27
; CURRENT FILING DATE: 1998-03-27
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                                                        Query Match:
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Best Local Similarity:
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EARLIER FILING DATE: 1987-04-03
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                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/09162484 Patent No. 6248724
                                                                                 SEQ ID NO 18
TYPE: DNA
ORGANISM: Homo sapiens
-09-162-484-18
                                                                                                  CURRENT FILING DATE: 1998-09-25
EARLIER APPLICATION NUMBER: 60/059,661
EARLIER FILING DATE: 1997-09-25
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                       APPLICANT: Phillips, M. Ian
APPLICANT: Mohuczy, Dagmara
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS TARGETED
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME MRNA AND METHODS O
FILE REFERENCE: UFLA:087/UFLA087P
CURRENT APPLICATION NUMBER: US/09/162,484
                                                             LENGTH: 4024
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                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Phillips, M. Ian
APPLICANT: Mohuczy, Dagmara
TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDE COMPOSITIONS TARGETED TO
TITLE OF INVENTION: ANCIOTENSIN CONVERTING ENZYME MRNA AND METHODS OF USE
FILE REFERENCE: UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UFLA:087/UF
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|TGCCAGGCAGCTGGCCACACGGGCCCCCTGCACAAGTGTGACATCTACCAGTCCAAGGAG 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-162-484-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 60/059,661
EARLIER FILING DATE: 1997-09-25
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3942
TYPE: DNA
ORGANISM: Rattus norvegicus
                                           2632 GATGGTCCCATTCCTGCCCACCTGCTAGGGAACATGTGGGCACAGACTTGGTCCAACATC
                                                                                                                                                                                                          2524 ------CAAGACCTGGAAAAACTATACCAGGAGCTGCAGCCGCTCTACCTGAAC
                                                                                                                        2572 CTGCATGCCTATGTGCGCCGCCTCCCTGCACCGCCATTATGGGTCTGAGTACATCAACCTG
                                                                                                                                                                                                                                                                                                                                                                            2422 TTCCCAAAGTACGTGGACTTCTCCAACAAGATCGCCAAGCTCAACGGCTACTCTGATGCA 2481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2188 GTTCAGAACGTGGACCGGGCAGTGCTGCCTCCCAACGAGTTAGAAGAGTACAACCAGATC
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279 TyrSerLeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetVal 298
                                                                                                                                                  240 LeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSer---TyrIleSerPro 258
                                                                                                                                                                                                                                                             220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 GluCysLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyTAsn 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 AlaGlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAla 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 GlnAsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 ThrIleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeu 39
                                                                   GlyGlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHis 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAATTGCTTTGGGTGTGGAAGAGCTGGCGAGACAAGGTGGGGAGAGCCATCCTTTCCCTTT 2421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTTGTCTGTCACTGGAGCCTGATCTGACAAATATAATGGCCACGTCCCGGAAATACGAA 2361
                                                                                                                                                                                                                                                                                                GGGGATTCCTGGAGATCCTCATATGAGTCCGATGACTTGGAG------
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US-09-440-325A-2

Sequence 2, Application US/09440325A

; Patent No. 6280994

; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.
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us-09-978-385-2 (1-805) x us-09-440-325A-2 (1-2082)
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LENGTH: 2082
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LOCATION: (1)...(2082)
OTHER INFORMATION: n = A,T,C or G
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241 HisAlaTyrValArgAlaLysLeuMetAsnAlaTyr---ProSerTyrIleSerProIle 259
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                                                                                                                      GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 240
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                                                              -CARGAYYTNGARMGNYTNTTYCARGARYTNMGNCCNYTNTAYYTNAAYCCN 774
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1774 YTNACNGGNGARWSNGARGTNWSNACNAAYGTNTTYATGACNTAYTTYAARCCNYTNYTN 1833
                                                                                                                                                                          1720 -----ytnytngcnytnaarytnggnwsnwarccntggccngargtnytnaaratg 1773
                                                                                                                                                                                                                                                          1660 WSNGGNCAYATGGGNCCNYTNCAYCARTGYGAYATHTAYAAYWSNAARATHGCNGGNAAR 1719
                                                                                                                              573 ValValGlyAlaLysAsnMetAsnValArgProLeuLeuAsnTyrPheGluProLeuPhe 592
                                                                                                                                                                                                                                                                                                                                         1600 MGNMGNTAYTTYYTNWSNYTNGTNYTNCARTTYCARTTYCAYGARACNYTNTGYAARGCN 1659
                                                                                                                                                                                                                                                                                                                                                                                                                       1540 WSNGARGARTTYGAYCCNGGNGCNAARTTYCAYTTYWSNGCNGGNGTNCCNTAYATH 1599
                                                                                                                                                                                                               553 LysLeuPheAsnMetLeuArgLeuGlyLysSerGluProTrpThrLeuAlaLeuGluAsn 572
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                                                                                                                                                                                                                                                                                               533 AlaLysHisGluGlyProLeuHisLysCysAspIleSerAsnSerThrGluAlaGlyGln 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               494 AspGluThrTyrCysAspProAlaSerLeuPheHisValSerAsnAspTyrSerPheIle 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    475 LYSLYSTrpTrpGlu---MetLYSArgGluIleValGlyValValGluProValProHis 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 ValGly-----LeuProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAsp 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           955 GTNCARCAYTGGAARCCNGARAARYTNATGYTNGARGARGCNGARACNTTYTTYACNTAY 1014
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 876-585:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08664596B Patent No. 5807703
                                                                                                                                                                                                                                                                                                                                                                                                                                                        . No.:
                                           302 TATCAAAGTTCACTTGCNTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                       242 ATTGAGGAACAGGCCAAGACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC 301
                                                                                                                                                                                                        182 ATGTCAAGCTCTTCCTGGCTCCTTCTCAGCCTTGTTGCTGTTAACTGCTGCTCAGTCCACC 241
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NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
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60 nAsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSerThrLeuAl 80
                                                               41 TyrGlnSerSerLeuAla-SerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValG1 60
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                                                                                                                                             21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPhe 40
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APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikki
APPLICANT: Bowman, Michael
TITLE OF INVENTION: SECRETED PROTE
TITLE OF INVENTION: ENCODING THEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/664,596B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
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CITY: Cambridge
STATE: Massachus
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SYSTEM: PC-DOS/MS-DOS
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LaVallie, Ed
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Indels:
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US-08-905-223-27
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GENERAL INFORMATION:
APPLICANT: Edwards
                                                                                                                                                                                                         Alignment Scores:
                                                                US-09-978-385-2 (1-805) x US-08-905-223-27 (1-848)
                                                                                                                                     percent Similarity:
Best Local Similarity:
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MEDIUM TYPE: Floppy Disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 848 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                               612 proTyrAlaAspGlnSerIleLysValArgIleSerLeuLysSerAlaLeuGlyAspLys 631
                                                                                                                                                                                                                                                         LOCATION: 32.73

LOCATION: 32.73

IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: SCORE 10.7
OTHER INFORMATION: SEG LWLLFFLVTAIHA/EL
                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Sapiens
DEVELOPMENTAL STAGE: F
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                                                                                                                                                                                                                                                                                                                                                                 TISSUE TYPE: kidney
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                                                                                                                                                                                                                                                                                                                             NAME/KEY: sig_peptide
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92101-3505
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501 West Broadway
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Duelert, Aymeric
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58.54%
42.44%
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                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER EILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
                                    ; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-247-155-27
   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/09247155A Patent No. 6312922
                                                                                                                                                                             SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: GENSET.021A
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bougueleret, Lydie TITLE OF INVENTION: Complementary DNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                             EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: 60/099,273
                                                                                                                                                                                                SOFTWARE:
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                                                                                                                          ORGANISM: Homo Sapiens
                                                                                                                                              TYPE: DNA
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                                                                                                             FEATURE:
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                                                                                                                                                             ENGTH: 848
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Query Match:

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Best Local Similarity:
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                                                                                                                                                                                                                                                                 Sequence 6, Application US/08157171 Patent No. 5736323
                                                                          APPLICANT: Soubrier, Florent
APPLICANT: Hubert, Christine
APPLICANT: COTVOL, Pierre
TITLE OF INVENTION: Agents and Pr
TITLE OF INVENTION: Enzyme
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 31
                                                                                                                                                                                                                                               GENERAL INFORMATION:
COMPUTER READABLE FORM:
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                                                CITY: Minneapolis STATE: MN
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                                 COUNTRY:
                 ZIP: 55402
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US-08-392-625-16
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08392625 Patent No. 5837485
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                      APPLICANT:
                APPLICANT: Kellner, Roland
TITLE OF INVENTION: Biosynthetic Process For The Preparation
TITLE OF INVENTION: Of Chemical Compounds
NUMBER OF SEQUENCES: 42
                                                                                                                                       APPLICANT:
CORRESPONDENCE ADDRESS:
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LENGTH: 192 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 TyrGluAspTyrGlyAspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyr 215
                                                                                                                                                                                                                                                                                                                                                                                               236 LeuTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyr---ProSer 254
                                                                                                                                                                                                                                                                                                                                                                                 153 CACATCAACCTGGAGGGGCCCATTCCTGCTCACCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hillson, Randall A. REGISTRATION NUMBER: 31,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 TATGTAGATGCAGGGGACTCGTGGAGGTCTATGTACGAGACACCATCCCTGGAG-----
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Wie, Thomas
                                                                                 Kupke, Thomas
Jung, G nther
                                                                                                                                    Kaletta, Co:
Klein, Cora
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Engelke, Germar
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 8700 base pairs
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FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 0652.0980002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/392,625
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                       111 AspLysSerLysArgLeuAsnThrIleLeuAsnThrMetSerThrIleTyrSerThrGly 130 ::: ||| ||| ||| ::: ||| ||| ::: 2867 AACGACGTTAAAAATTTAGAAAAG---AATAATACAGTTTCTAAAATCAATGCG----- 2867
                                                                                                                                                                                                              2754 GCATTTTTAAAAGAAAAG-----
                                                                                                                                                                                                                                                                                                2742 TCTAATAACATT-----
                                                                                                                                                                                                                                                                                                                                                                              2682 AAGCAATTGCTCTCAGATATAAATGGATTTGGCTATCCCAAAAAAGACAGTTATAGTTTT 2741
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2562 ATTAGTGAAGCAGCATATATTCTCTGGTTATTATCTCCTAATCATTTTGGTACAAAAACT 2621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Sterne,
STREET: 1100 New 1
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
131 LysValCysAsnProAspAsnProGlnGluCysLeuLeuLeuGluProGlyLeuAsnGlu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 20005
                                                                                                                                                                                                                                   71 AlaPheLeuLysGluGlnSerThrLeuAlaGlnMetTyrProLeuGlnGluIleGlnAsn 90
|||||||||||||||
                                                                                                                                                                                                                                                                                                                                     51 AsnThrAsnIleThrGluGluAsnValGlnAsnMetAsnAsnAlaGlyAspLysTrpSer 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGlu----- 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr 20
                                                                                                                                                                  LeuThrValLysLeuGlnLeuGlnAlaLeuGlnGlnAsnGlySerSerValLeuSerGlu 110
                                                                                                                                                                                                                                                                                                                                                                                                                   -----AlaGluAspLeu-----PheTyrGlnSerSerLeuAlaSerTrpAsnTyr 50
                                                                                                                           -----TATTTGCTTGCAATTCAAAATAACAGCCATATTGAAATAACAGAA 2816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
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                                                                                                                                                                                                                                                                                                  2753
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3818	74 TGGTTTTCAATTCATTTAAGTATTCCTAAAACATACCAAGAT	Db
437		Qy
3773	ATACCTAAAAATAGAAATAAGCACTT	DЬ
419	hrProLyshisLeuLys	Qy
3713	::: ::: :::	ДЪ
409	luGlyPheHisGluAlaValGlyGluIleMetSer	Qy
3653	TTATCAAT	Дb
397	nProPheLeuLeuArgAsnGlyAlaAsn	ОУ
3593	3534 ATTATTGCTTTTGGAGATAATCGATTGCTATTAAATTTATTAAATGACAAGCATCTCATT	ДĎ
386		Qy
3533	GCATATTCCAAAAGATGTA	Db
383	HisHisGluMetGlyHisIleGlnTyrAspMet	Qy
3476	ACTGAA	Db
363	LeuMetCysThrLys	Qy
3425	3366 ACTGAAGAAGGCATTGACTCATTACCTTTTTGTCCAAGAATTATTTAT	Db
343		Qу
3365	TTTTAAGAGAAATTTCATTTGAAAAAAAAAATTTATACAACCTATA	Дb
337	AspProGly	Qy
3305	3246 AAACATGATTCAAGAATTGTATTCGTATCTAATTCAATGTTTAATTATGAGTTTGGATCT	Db
326		Qy
3245	3186 ATAGATATAAATGACATATTTATTGGAGCTACATTTAACAAACTTTATCTATATTCTGAA	Db
310	.laMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGlu	Qy
3185	3138AATAGAATATATAATACTTGTTTAAATTTAAATTTACCTAAAAAGTGAT	Дb
290	lnLysProAsn	Qy
3137	3081 ATAAGCCAATTAAATGAAGGTCCTCTTAACTCAAGAAATGTAAATATTTTGAATAAT:	Db
270	Met	Qy
3080	3045CATTACAATAATTACATGAATGAAAATGGTTTAGAA :	DЬ
250	ysProLeuTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsn	Qy
3044	3012AAAAAAATCAATTACAAAAAAAAAATAGTGCAT	Db
230	ThrPhe	Qy
3011	2955 GGATCTTTAATGCCGGTGCAACTTTTGGAAGGTTTACGGGAAATTTCAATATAAAG	Db
210	TrpArgGlyAspTyrGluValAsn	Qy
2954	2904GGAAATTCAATAAAAGGTTATGAGGATTTTGCCGTGATAAGTCCAATATTA	Db
190	LeuTyrGluGluTyrValValLeuLysAsnGluMet	Qy
2903	83 ATATATAGTGAGATATTTT	Db
170	${\tt eMetAlaAsnSerLeuAspTyrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSer}$	Qy
2882	2868CCTGTTTCAACTGAA	Db

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4251 TTATATCGTAGTAATGAC-----
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                                                                                                                                                                                                         ATTGGCAGTTTT---ATAAACATGCGTTGTAATAGAATATTCGGTATTAATCCT 4490
                                                                                                                                                                                                                                                       AsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLeuGlyIleGlnPro 729
                                                                                                                                                                                                                                                                                                   ATTTTAGAAAATCTTAAAAAGACACTACAAAAAAGCTTATATACTTCACGTTCTAGGATA
                                                                                                                                                                                                                                                                                                                                                                                            TATGAAATTTTAAAAAAAGAATTTCCGAATCTTCATGAATTTCTATTTAATAAAATTAGT 4379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---AAAAATTTATTAGCTAAACTT-------ACCAATCCTAAAAATGAC 4319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgGlnTyrPheLeuLysValLysAsnGlnMetIleLeuPheGlyGluGluAspValArg 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSerSerValAlaTyrAlaMet 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProTyrAlaAspGlnSerIleLysValArgIleSerLeuLysSerAlaLeuGlyAspLys 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheThrTrpLeuLysAspGlnAsnLysAsnSerPheValGlyTrpSerThrAspTrpSer 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTATCGTTGCT-----ATATCAATAGATTTTTTATTAGATTATTAGAA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnLysLeuPheAsnMetLeuArgLeuGlyLysSerGluProTrpThrLeuAlaLeuGlu 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaAlaLysHisGluGlyProLeuHisLysCysAspIleSerAsnSerThrGluAlaGly 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATTATTGCTTATTAAATAGTGAATTATATGACTATTCTATAGTTGATTATGTTCCTGAA 4046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ThrArgThrLeuTyrGlnPheGlnPheGlnGluAlaLeuCysGln 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysAspProAlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyr---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATTTTTTTACATAAAATTTAAAGAAGAT------GAAGATTTTATAAAA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PheLeuLeuLysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGlu 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValAlaAsnLeuLysProArgIleSerPheAsnPhePheValThrAlaProLysAsnVal 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----CTCTCAAATTTATTCTTTCATAAAAAATTGGAAA 3986
                                                                                                                                                                                                                                                                                                                                            ------ArgThrGluValGluLysAlaIleArgMetSerArgSerArgIle 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---ATTAATAAAAGTGAGAAAGAAGAAATTTTAATTAATGCG-----GAAGAT 4250
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DB:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                             US-09-978-385-2 (1-805) x US-08-466-961A-16 (1-8700)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-466-961A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Esmond, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 30-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: US 08/392,625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Biosynthetic Process for the Preparation TITLE OF INVENTION: Chemical Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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2682 AAGCAATTGCTCTCAGATATAAATGGATTTGGCTATCCCAAAAAAGACAGTTATAGTTTT 2741
                                                                                                                                                                                                                                                                                                                                                                                                                                             No. :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C.
                                              36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/784,234 FILING DATE: 31-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGlu--
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                                                                                         ATTAGGAATTATCACGAATTTTTTATGGATAAATATGGATTTGAACAACTAGTAAATTTA 2681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8700 base pairs
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1100 New York Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U.S.A.
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Jung, G nther
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Kaletta, Cortina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kellner, Roland
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                                           --AlaGluAspLeu-----PheTyrGlnSerSerLeuAlaSerTrpAsnTyr
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Matches:
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SerAspIleIlePro-----

AGAGAATAT - - - - -

US-08-466-961A-16

Sequence 16, Application US/08466961A Patent No. 5843709 GENERAL INFORMATION:

APPLICANT:

APPLICANT:

G tz, Friedrich Schnell, No. 5843709bert Entian, Karl-Dieter RESULT 14

4440

δÃ В γQ

	eGlnTyr TCCAAAA			327	311AlaGluLysPhePheValSerValGlyLeuProAsnMetThrGlnGly 326 ::: 3246 AAACATGATTCAAGAATTGTATTCGTATCTAATTCAATGTTTAATTGAGTTTGGATCT 3305	nArgIl :: TTATCT	271 TrpGlyArgPheTrpThrAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsn 290	251 AlaTyrProSerTyrIleSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMet 270	MetAsn ::: TTAGAA		191 AlaArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrpArgGlyAspTyrGluValAsn 210 	171 GluValGlyLysGlnLeuArgProLeuTyrGluGluTyrValValLeuLysAsnGluMet 190	151 IleMetAlaAsnSerLeuAspTyrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSer 170 	131 LysValCysAsnProAspAsnProGlnGluCysLeuLeuLeuGluProGlyLeuAsnGlu 150 2868CCTGTTTCAACTGAA 2882	111 ASPLYSSETLYSÄTGLEUÄSNTHTILELEUÄSNTHTMELSETTHTILETYTSETTHTGLY 130 :::	91 LeuThrValLysLeuGlnLeuGlnAlaLeuGlnGlnAsnGlySerSerValLeuSerGlu 110	71 AlaPheLeuLysGluGlnSerThrLeuAlaGlnMetTyrProLeuGlnGluIleGlnAsn 90 ::: 2754 GCATTTTAAAAGAAAAG	51 AsnThrAsnIleThrGluGluAsnValGlnAsnMetAsnAsnAlaGlyAspLysTrpSer 70 ::: 2742 TCTAATAACATT
l oy	Qy Db	Оу	Qy	ДУ	Db X	O Db Qy	Qy Db	Оу	Qy dd	Qy Db	Qy Db	Оу	Db Db	Оу	Qy Db	Qy	Фу	 D Ø
9 692 SerAspIleIlePro 696	y 672 ValAlaAsnLeuLysProArgIleSerPheAsnPhePheValThrAlaProLysAsnVal 691	y 652 ArgGlnTyrPheLeuLysValLysAsnGlnMetIleLeuPheGlyGluGluAspValArg 671 ::: b 4272 AGAGAATAT4280	y 632 AlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSerSerValAlaTyrAlaMet 651 	y 612 ProTyralaAspGlnSerIleLysValArgIleSerLeuLysSerAlaLeuGlyAspLys 631 :::::: ::: :: ::: b 4203ATTAATAAAAGTGAGAAAGAAGTTTTTAATTAATTA	4202	572 AsnValValGlyAlaLysAsnMetAsnValArgProLeuLeuAsnTyrPheGluProLeu ::::	y 552 GlnLysLeuPheAsnMetLeuArgLeuGlyLysSerGluProTrpThrLeuAlaLeuGlu 571	532 AlaAla 4047 GTATAT	y 517ThrargThrLeuTyrGlnPheGlnPheGlnGluAlaLeuCysGln 531 :: :: :: :: :: :: :: :: :: :	y 498 CysAspProAlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyr 516	y 478 TrpGluMetLysArgGluIleValGlyValValGluProValProHisAspGluThrTyr 497 ::: b 3924 TTAAGATTATTAAGAGAA	w	y 438 PheLeuLeuLysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGlu 457	y 420SerIleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsn 437	y 410LeuSerAlaAlaThrProLys	398 GluGly 3654 GAATCT	387 3594	384 AlaTyrAla384 AlaTyrAla

B Qy В Qy B Q В Qy В Qy 밁 δÃ В $Q_{\underline{Y}}$ В δÃ ₽ Ωy В Qy 밁 Qy Ъ Qγ 뫄 γQ 밁 Qy DЬ QΥ В Qy В

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Best Local Similarity:
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US-08-645-193B-18
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                                                                                                                                                                                                                                                                                                                                                   US-08-645-193B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REGISTRATION NUMBER: 0652
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/08645193B
Patent No. 5962253
GENERAL INFORMATION:
APPLICANT: Kupke, Thomas
APPLICANT: Kupke, Friedrich
APPLICANT: Kempter, Christoph
APPLICANT: Jung, Gunther
                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: bot
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 8700 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/645,193B FILING DATE: 13-MAY-1996 CLASSIFICATION: 435 ATTORNBY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4380 ATTTTAGAAAATCTTAAAAAGACACTACAAAAAGCTTATATACTTCACGTTCTAGGATA 4439
2622 ATTAGGAATTATCACGAATTTTTTATGGATAAATATGGATTTGAACAACTAGTAAATTTA 2681
                                                                          2562 ATTAGTGAAGCAGCATATATTCTCTGGTTATTATCTCCTAATCATTTTGGTACAAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jung, Gunther
TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
TITLE OF INVENTION: Catalyzed by Flavoprotein EpiD
NUMBER OF SEQUENCES: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4440 ATTGGCAGTTTT---ATAAACATGCGTTGTAATAGAATATTCGGTATTAATCCT 4490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4320 TATGAAATTTTAAAAAAAGAATTTCCGAATCTTCATGAATTTCTATTTAATAAAATTAGT 4379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                      21 IleGluGluGlnAlaLysThrPheLeuAspLysPheAsnHisGlu------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
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                                                                                                            1 MetSerSerSerTrpLeuLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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153
120
258
310
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                                        <u>3</u>5
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383	ValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGlnTyrAspMet	364	Oy	
3476	TTAAAACCAGCTACTTGGAAAATAAATTCAGAAATGTTTTCTGAAACTGAA	3426	Db	
363	euMetCysThrL 	344	Qy	
3425	ACTGAAGAAGGCATTGACTCATTACCTTTTTGTCCAAGAATTATTTAT	3366	Db	
343	AsnValGlnLysAlaVal	338	Qy	
3365	::: ::: GAATTATACAAATTTTAAGAGAAATTTCATTTGAAAAAACAAAATTTATACAACCTATA	3306	Db	
337	PheTrpGluAsnSerMetLeuThrAspProGly	327	Qy	
	AAACATGATTCAAGAATTGTATTCGTATCTAATTCAATGTTTAATTATGAGTTTGGATCT	3246	Db	
326	AlaGluLysPhePheValSerValGlyLeuProAsnMetThrGlnGly	311	νQ	
		3186	Db	
310		291	Q 5	
290	<pre>TrpGlyArgPheTrpThrAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsn</pre>	271	Qy	
3137	ATAAGCCAATTAAATGAAGGTCCTCTTAACTCAAGAAATGTAAATATTTTGAATAAT	3081	Db	
270	AlaTyrProSerTyrIleSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMet	251	Qy	
3080	CATTACAATAATTACATGAAAAAAAAGGTTTAGAA	3045	Db	
250	GluGluIleLysProLeuTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsn	231	Qy	
3044	AAAAAAATCAATTACAAAAAAGTAGTGCAT	3012	Db	
230	GlyValAspGlyTyrAspTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPhe	211	Qy	
3011	GGATCTTTAATGCCGGTGCAACTTTTGGAAGGTTTACGGGAAATTTCAATATAAAG	2955	Db	
210	AlaArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrpArgGlyAspTyrGluValAsn	191	Qy	
2954	GGAAATTCAATAAAAGGTTATGAGGATTTTGCCGTGATAAGTCCAATATTA	2904	Db	
190	GluValGlyLysGlnLeuArgProLeuTyrGluGluTyrValValLeuLysAsnGluMet	171	Qy	
2903	ATATATAGTGAGATATATTT	2883	Db	
170	IleMetAlaAsnSerLeuAspTyrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSer	151	Qy	
2882		2868	Db	
150	LysValCysAsnProAspAsnProGlnGluCysLeuLeuLeuGluProGlyLeuAsnGlu	131	ρy	
2867	HIT HIT STANDART TAGARANGARTARTACAGTTTCTARARTCAATGCG	2817	Db	
130	AspLysSerLysArgLeuAsnThrIleLeuAsnThrMetSerThrIleTyrSerThrGly	111	УО	
2816	TATTTGCTTGCAATTCAAAATAACAGCCATATTGAAATAACAGAA	2772	Db	
110	LeuThrValLysLeuGlnLeuGlnAlaLeuGlnGlnAsnGlySerSerValLeuSerGlu	91	Qy	
2771	GCATTTTTAAAAGAAAAG	2754	DЬ	
90	AlaPheLeuLysGluGlnSerThrLeuAlaGlnMetTyrProLeuGlnGluIleGlnAsn	71	Qу	
2753	TCTAATAACATT	2742	ממ	
70	$As n {\tt ThraselleThrGluGluAsenValGlnAsenMetAsenAsenAlaGlyAseLysTrpSer}$	51	Qy	
2741	AGCAATTGCTCTCAGATATAAATGGATTTTGGCTATCCCAAAAAAGACAGTTATAGTTTT	2682	Db	
50		36	Qy	

691	ValAlaAsnLeuLysProArgIleSerPheAsnPhePheValThrAlaProLysAsnVal	672	Ωу
671 4280	ArgGlnTyrPheLeuLysValLysAs ::: AGAGAATAT	652 4272	ДУ Db
651 4271	AlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSerSerValAlaTyrAlaMet	632 4251	Оу
4250	ProTyrAlaAspGlns :::::! ATTAATAAA	612 4203	Qу Дъ
4202		4202	Db
611	${\tt PheThrTrpLeuLysAspGlnAsnLysAsnSerPheValGlyTrpSerThrAspTrpSerDheValGlyTrpSerD$	592	Qy
1 591 4202	ASnValValGlyAlaLysAsnMetAsnValArgProLeuLeuAsnTyrPheGluProLeu:::	572 4158	Ωу
1 571 1 4157	GlnLysLeuPheAsnMetLeuArgLeuGlyLysSerGluProTrpThrLeuAlaLeuGlu 	552 4107	Ωу
4106	ດ :	4047	DP AA
	GATTATTGCTTATTAAATAGTGAATTATATGACTATTCTATAGTTGATTATGTTCCT	3987	B B
531	ThrargThrLeu	517	Qy
- 516 1 3986	CysAspProAlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyr	498 3954	ОУ
r 497 r 3953	TrpGluMetLysArgGluIleValGlyValValGluProValProHisAspGluThrTyr::: 	478 3924	Оγ
- 3923		3879	B 2
. (4)	TTTATTCAAGATTATCTATTACCATTTATAACGGAATTAAAAGTTAATAATTTTATTAA	3819	g B
1 457		438	Qy
1 437 1 3818)SerIleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsn 	420 3774	рb
- 419 T 3773	LeuSerAlaAlaThrProLys	410 3714	рβ
- 409 A 3713	GluGLyPheHisGluAlaValGlyGluTleMetSer	398 3654	αq
n 397 3653	⊳ .	387 3594	B 8
w	 ATTATTGCTTTTGGAGATAATCGATTGCTATTAAATTTATTAAATGACAAGCATCTCAT	3534	ф
- 386	AlaTyrAla	384	Qy
: A 3533	ARTIGGTTAAATAGGTTCGCAACTATTAGAGAAAAATGGCATATTCCAAAAGATGT	3477	ф

RESULT	Qy	Оу	Qy	Оу	Qy Db	us-09	Alignment Pred. No. Score: Percent S Best Loca Query Mat DB:	Db OY OY OY OY OY OY Db Db INSTITUTE SERVITE SE
r 17	258 ProIleGlyCysLeuProAlaHisLeuLeu 267 :::	239 HisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSer 257 :::	219 ArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGlu 238 ::: :::	199 TyrGlyAspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSer 218	186 LeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAsp 198	-978-385-2 (1-805) x US-09-280-116-114 (1-789)	Alignment Scores: 0.000133	Ob 4281AAAAATTTATTAGCTAAACTT

US-09-453-702B-1/c

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                                                                                                                                                                                                                                                                                                                                                                                              Query Match:
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Best Local Similarity:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (608) 251-9:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6506
TYPE: nucleic acid
3628 GCAGGGAAAAACAAAATTAAACTTGCATTGCAAAAACCGGATAAAGTTACTTTGGCGTCCA 3569
                                                                                                                                                            3778 ACATTTATTCTCACACCGCCAGTAAGTCGTGTAGCAGGTGGTTCTGGCCAACAACTTAAA 3719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.:
                                     65.AlaGly---AspLysTrpSerAlaPheLeuLysGluGlnSerThrLeu------ 79
                                                                                                                    45 LeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGlnAsnMetAsnAsn 64
                                                                                                                                                                                               25 AlaLysThrPheLeuAspLysPheAsnHisGluAlaGluAspLeuPheTyrGlnSerSer 44
                                                                                                                                                                                                                                                                              5 SerTrpLeuLeuSerLeuValAlaValThrAlaAlaGlnSerThrIleGluGluGln 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: RADABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-LOS/MS-DOS
SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILLING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: WI
COUNTRY: US
ZIP: 53701-2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Madison
                                                                               -----CTAAATGTTCTGGATATCCCTCCAAACAATCCACAAAT 3629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burland, Valer
Perna, Nicole T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plunkett, Guy
Welch, Rod
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120.50
32.57%
19.29%
2.81%
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08) 251-9166
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
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65	346 ProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMetCysThrLysValThr 3	Qy
582	41 TGGTCGCAGATATTAAGCACAGTTCAGATAGGAGAAAATTACACATCCTCACTCA	Db
45	snValGlnLysAlaValCysHis 3	Qy
	AGCAAACCCGATGATATGAAAGGCACATGGCAAAGTAATACTCTTTACCTGGAACATGGC 2	ДĎ
37	etThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGly 3	Qy
702	2761 GGCCGATTTAACAGTGGATTAAATTTATTTAGTTGGCAGTTACACTCTGATGCCAGCTAT 2	DЪ
20	320 3	Qy
762	2821 TATAATTTAAGTCAGTATCGCTCTTATGACAGCAATAATAACAGTAATACAGCCAGTTAT 2	рь
320	318 ValGlyLeu 3	Qу
2822	CGCGGCATTGATGCTTTTTATACCTCC	Дb
317	¶TrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSer	Qy
2867	2926 CACCGACTAAATTTAACAGTACCACAGGCGTATATCAATGAACTTGAAAGAGGTTACGTT 2	Db
299	288LysProAsnIleAspValThrAspAlaMetValAsp 2	Оу
2927	TGGGATATCAGTGAA	DЬ
287		Qy
2987	3046 CTGCCTAAGGTGCTACCTAACCAAACTGGGGGTAAAGACCGGTAACCTCAATACAGAAGAT ;	Db
277	;	Qу
3047	_	Db
261	TyrlleSerProlleGlyCys	Qy
3101	Ċ	рь
244	isLeuHisAlaTyrVal	Qy
3158	GAATATCAT	DЬ
229	GluHisThr	Qy
3194		Db
209	Val	Qy
N	::: ::: AGTCATGTTAAGGACGACACGATGGGTCGCTGCTATT	Db
9	DLeuTyrGluGluTyrValValLeuLysAsnGluMetAlaArgAla	Qy
ω	:: :: ::: ::: ::: ::: ATGATTACGGGAATAACATCCATAGTAAA	DЬ
175	pGluSerTrpArgSerGluValGlyLysGln	Qу
3374		Δb
155	luCysLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSer	Qy
3434	 AACGTGAA	Db
37	snThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAsp	Qy
3476	::: CAATAAACAACGAAACAGCCAAC	Db
17	aLeuGlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsn	Qy
3509	3568 AGCGGAATAGCTCCGGTAGATAAAAAAAGCCTTTCTCAATTAAATATCAAAAAAGAAAAAT	Db
97	80 AlaGlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeu	Qy

rAlaMetArgGlnTyrPheLeuLysValLysAsnGlnMetIleLeuPh 665 	Мe	64	Qγ
TATACHTICICIGC 1/04	7	171	뫄
pLysAlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSe 64	sSerAlaLeuGlyAspLys	62	Qy
pTrpSerProTyrAlaAspGlnSerIleLysValArgIleSerLeuLy 625 CTGGCAA	5 YTTPSerThrAspTrpSerF ::: 5 TTATTCCAATAGCTGGCAA-	60! 174!	Db dd
ь с	TTAC-	1787	90 40
rececifiedeedaa 1/0		1834) B
laLys	н	56	y Qy
LEUTHEASHMELLEUAT 9 LEUGT AUF SEEL GEGET AUGUST AUG	н н	1883	Db 68
л		1934	מ נ
GlyProLeuHisLysCysAspIleSerAsnSe	uAl	527	VQ V
ш	C	1994	B
nPheGlnGl 527	E	520	Qy
ACGAAGGTACGAGCTATCAGGTCGCCTATAATAATATCTAGTACAAACGGC 1995	TATAACAC	2054	В
AsnAspTyrSer	rLeuPheHisValSer	502	Qy
 GCCATCTCTTTTGACGCTACACGATCGAGTAGTAAGTTA-AATAATGA 2055	ACACCGCTGGGTGCCATC	2113	Db
lProHisAspGluThrTyrCysAspProAlaSe 502	lValGluProValPr	487	ρy
		2127	Db
lnTrpMetLysLysTrpTrpGluMetLysArgGluIl	uIleProLysAspG	467	Qy
GATAACTATAATGCTATAACTCTGG 2128	ACGATTTATCCG	2164	Дb
ProPheThrTyrMetLeuGluLysTrpArgTrpMetValPheLysGlyGl 467	ThrLeu-	449	ρy
::::: 	GACTTTCTCGAGGCAAATT	2224	Dβ
leAsnF	AsnGluThrGluIleAsnF	432	γ0
 ATTTTATCGCCGGACGCAGTAAGATATATGGTGTAAAGAATCAGGAG 2225	::: : :: ATTTCAAATTTCGATTTT	2284	ρь
spPheGlnGluA	spPhe	423	Qy
TTTTTGGTGCCCTACTCTTCCGTGCCTAACATGCTGCAACCTGGT 2285	::: AGTGTTCGTTCC	2341	В
SerAlaAlaThrProLysHisLeu	GluIleMetSerLeu	406	Qy
 CGGGCAGCGGCTCTGATCTCGATGTCAGCATAAAGGAAGCAGATGGC 2342	GATTTGCAACTCTCGGGCAGC	2401	Дb
lyPheHisGlu	AsnGlyAlaAsnGluGly	394	Qy
CATCATI	ATC	2461	В
iisIleGlnTyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArg 393	HisGluMetGlyHisIleGlr	374	QΨ
CACCTTTAGTACAAGGTGTTGCGCAAAGTAATGCCTTGATAAACGGTT 2462	MetAspAspPhe	366 2521	B 6
3 6	GACTCTCTGAGATTTAGCGGF	- α	DЬ
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N, N				RESU US-0; ; Se ; Pa ; G	Db	Qу	Оу	Оy	Qy Db	Db Qy	Qy	Фр	Оу	Db
APPLICATION UNMBER: FILING DATE: FITING DATE: ATTORNEY/AGENT INFORMATION: NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PB340P1 TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 45: SEQUENCE CHARACTERISTICS: LENGTH: 11384 base pairs TYPE: nucleic acid STRANDEDNESS: double	RATING SYSTEM: TWARE: ASCII TO NT APPLICATION I LICATION NUMBER LICATION OATE: SSIFICATION: 4:	ORM: kette, 3.50 inch, tra 486/33	RESPONDENCE ADDR DDRESSEE: Human TREET: 9410 Key	E 440 E	1370 TATTAGTAGT 1361	800 pValGlnThr 803	780 oTyralaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAs 800	765 eArgAspArgLysLysAsnLysAlaArgSerGlyGluAsnPr 780 : ::::::::	745 1PheGlyValValMetGlyValIleValValGlyIleValIleLeuIlePheThrGlyIl 765 ::: ::: 1505 TTATGGTATATAT	725 uGlyIleGlnProThrLeuGlyProProAsnGlnProProValSerIleTrpLeuIleVa 745 1543 -GGAATTACTGGCATAGCCGGTGAACATGATCAGTTAAA 1506	705 gMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLe 725	685 IThralaproLysasnValSerAspIleIleProArgThrGluValGluLysalaIleAr 705 ::::	665 eGlyGluGluAspValArgValAlaAsnLeuLysproArglieser/neksniphera oo 	

045	TyrSerLeuThrValProPheGlyGlnLysPro:::: ::::: :::: TTCGCTTTAGAGCATGCTTATGGCCGACCAGAGGAGTTT	105	D 09
271 10518	252 TyrProSerTyrIleSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrp 2	10:	Дb
251 10557	232 GluIleLysProLeuTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAla :	10:	p Q
231 10581	212 ValAspGlyTyrAspTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGlu;	10	D dd
211 10641	ALGALAMHISTYTGILASPTYTGIASPTYTTYPÄTGGIYASPTYTGILVAIASNGIY	10	P 5
191 10680	VALULY MYSGINGUMATGPTOLEUTYTGIUGIUTYTVALVAILEULYSASNGIUMEtAla ::	10	}
171 10704	SETEUASPTYTASHGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu	10	P P 9
154 10758	135 ProAspAsnProGlnGluCysLeuLeuGluProGlyLeuAsnGluIleMetAlaAsn	10	0 dd
134 10785	115 ArgLeuAsnThrIleLeuAsnThrMetSerThrIleTyrSerThrGlyLysValCysAsn ::::::	10	dg dy
114 10815	95 LeuGlnLeuGlnAlaLeuGlnGlnAsnGlySerSerValLeuSerGluAspLysSerLys ::: ::: 856AAATATCATGTCACACGTCAAAATGGTCATCAACTGATGAAG	10	dq VQ
94 10857	78 ThrLeuAlaGlnMetTyrProLeuGlnGluTleGlnAsnLeuThrValLys ::: ::: 883 AATATGGCTCAAGAAGGGCATATTTAC	10	ρ γ
77 10884	58 AsnValGlnAsnMetAsnAsnAlaGlyAspLysTrpSerAlaPheLeuLysGluGlnSer :::	10	Db Qy
57 10932	48 TrpAsnTyrAsnThrAsnIleThrGluGlu	0 10	dg Qy
47 1099	051 C#	0 11	무성
42 1105	23 GluGlnAlaLysThrPheLeuAspLysPheAsnHisGlu	. 5 11	45 d
	978-385-2 (1-805) x US-08-961-52	3-09-	Sn
		er ed	Al Sc Sc Be Be DB
	TOPOLOGY: linear -961-527-45	S-08	g :-

556	43AspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsn	0у 5	
9565	24 TATTTCGCTTCTCAGCTAAACCAGTTTTACAAAGATCATCGCTGTCTGT	v	
542	40	>	
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539		Оу :	
9685	9744 TGTCACCCTGGTAAGAAATTGCTCTTCATGGGTAGCGAATACGGTCAATTCCTAGAATGG	Db 9:	
535		Qy	
9745	ATT	Db 9.	
529	Ĕ	Qy	
9781	AGATCGTTACAATCAA	Db 9:	
509	nAsp	Qy	
9841	858 TTGCCATTCTCGCACGAT	Db 9	
494	475 LysLysTrpTrpGluMetLysArgGluIleValGlyValValGluProValProHisAsp	Qy	
9859		Db 9	
474	470LysAspGlnTrpMet	Qy	
9919	978 TGGAACATGGGCTGGAATGAATGATATCCTCCGTTTCTACGAAGAAGATCCGATCTATCGT	Db 9	
469	459 TrpArgTrpMetValPheLysGlyGluIlePro	Qy	
9979	.0029 ATCAAGATTACGGGAATGAAAGAGATTGGTGGTCTAGGATTTGACTACAAA	Db 10	
458	439 LeuLeuLysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLys	Qy	
10030	.0071TATCCAGATGTGATGATGATGCAGAAGAAAGTTCGTCTGCG	Db 10	
438	419 LysSerIleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPhe	Qy	
10072	.0110 TATTTCCTTCAGCGCTTGAATGAGGTTATTAAGTTAGAA	Db 10	
418	401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeu	Qy	
10111	0158CCATGGACACCTAATAAAGATGGCGGAAATCTCAACTATGAAGGTTAT	Db 10	
400	385 TyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe	Qy	
10159)218 TIGGATGGTATICGTGTGGATGCTGTTAGCAACATGCTCTATTTGGACTATGATGATGATGCT	Db 10	
84	370LeuThrAlaHisHisGluMetGlyHisIleGlnTyrAspMetAla	Qy	
0	CCTTCTTAATTTCTTGCATTAAGCATTGGATTGATGTCTATCA	Db 10	
	353 LysGlyAspPheArgIleLeuMetCysThrLysValThrMetAspAspPhe	Qy	
0	332 GACCATAATAAGGCTCATAACCATGGTTGGGGTGCCCTTA	Db 10	
352	338 AsnValGlnLysAlaValCysHisProThrAlaTrpAspLeuGly	Qy	
10333	.0391 TTACCATCAACGATGATGCCTTA-GCCTATTATGATGGGACACCGACTTTTGAATACCAA	Db 10	
	١.	Qу	
0	.0406TGGGTACCAGTCACT	Db 10	
	300 GlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGly	Qy	
10407	0457 CAAGATTTTGTCGAGGAGTGTCATACCCATAATATTGGGGTTATTGTGGAC	Db 10	
299	290AsnIleAspValThrAspAlaMetValAsp	Qy	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08157171 Patent No. 5736323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                         TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9564 ACCAGCTATGATGGTATTGAAATCATTGATGCGGATAATCGAGACCAGAGTGTTCTTTCC 9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9444 GAGCGGAAAGATTTTACAATCGGACTACCCGTTGCAGGAATTTACGAAGAAGTATGGAAT 9385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9504 TTTATTCGTAAGGGTAAAAAGGGAGAAATGTTAGTCTGTATCTTTAATATGGTACCTGTT 9445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9261 GTATGGAAAATCAAACGTCGCTTGAAATCTACTAAAACCGTCACAAATAAAAACCAAAAA 9202
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 653 GlnTyrPheLeuLys-----ValLysAsnGlnMetIleLeuPheGlyGluGluAspVal 670
  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     671 ArgValAlaAsnLeuLysProArgIleSerPheAsn 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 90 Soutn /
                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                  LENGTH: 144 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/157,171 FILING DATE: 24-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Merchant & Gould STREET: 90 South 7th Street, 3100 No. 5736323west Center
                                                                                                                                                               TELEPHONE:
                   TOPOLOGY:
                                                                                                                                                                                                                                                    NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrAlaAspGlnSerIleLysValArgIleSerLeuLysSerAlaLeuGlyAspLysAla 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetLeuArgLeuGlyLysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAla 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAT---AATCAAACTGTTCAAACGCAAGAAGGACTA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSerSerValAlaTyrAlaMetArg 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTGAGTTGGAAGAG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysAsnMetAsnValArg-----ProLeuLeuAsnTyrPheGluProLeuPhe--- 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TGGAAAGATTATGAGCAGACCTTAACCTTTACCCTACCGGCTATGGGAGCAAGT 9262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55402
                                                                                                                                                                                                                                                    Hillson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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Hubert, Christine
                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                   linear
DNA (genomic)
                                                                                                                                                                                                                                                  Randall A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Agents and Procedures for the Study of the Genetic Polymorphism of the Angiotensin I Converting
                                                                                                                                                                                                           8076.103USWO
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US-08-961-527-115/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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                                                                                                 US-08-961-527-115
Percent Similarity:
Best Local Similarity:
                                  Score:
                                                  Pred. No.:
                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 115, Application US/08961527
Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                            TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
CLONE: Exon 17
                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PB TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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TyrSerThrGlyLys 131 Db 1888 AAAATTTCGTTAATAAGGAGAA 2525 Qy 427 | GATAGAÄCÄTTGCATTCAGAATA 2801 Qy 359 laPheLeuLysGlu 75 | GATAGAÄCÄTTGCATTCAGAATA 2801 apheleu | GATAGAÄCÄTTGCATTCAGAATA 2801 1 1 1 1 1 1 1 1 1 | GATAGAÄCÄTTGCATTCAGAATA 2801 Qy 359 lapheLeuLysGlu 75 | GAPTAGAÄCÄTTGGAATTA 2801 Qy 359 laPheLeu
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 | GAAGTTTTGAGGAT 2645 GAAGTTTTGAGGAT 2645 QY 419 AAATTTCGTTAGATTATACGAG 2585 AAAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAATAAGAAA 2525 ATCTGCACTTTAATAAAGAAAGAAA 2525 ATCTGCACTTTAATAAAGAAAGAATA 2495 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | GAAGTTTTGAGGAT 2645 QAAGT | GAAGTTTTGAGGAT 2645 QY 419 TYPESTTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TYPESTTAGAGAAA 2525 ATCTGCACTTTAATAAAGGAAA 2525 EUGluProGlyLeuAsnGluIle 151 :: | GAAGTTTTGAGGAT 2645 QY 419 TyrSerThrGlyLys 131 AAATTTCGTTAATAATCGAG 2585 AAATTTCGTTAATAATAATCGAG 2585 ATCTGCACTTTAATAATGAAGAAA 2525 ATCTGCACTTTAATAATGAAGAAA 2525 COY 427
 | GAAGTTTTGAGGAT 2645 GAAGT | GAAGTTTTGAGGAT 2645 QAAGTT | GAAGTTTTGAGGAT 2645 QAAGTT | GAAGTTTTGAGGAT 2645 QY 419TYPSerThrGAYLYS 131TYPSerThrGAYLYS 131 AAATTTCGTTAATAATGAAG 2585 ATCTGCACTTTAATAATGAAGAAA 2525 EUGLUPTOGLYLEUASGGAGAA 2525 EUGLUPTOGLYLEUASGGAGAA 2525 TA

 | GAAGTTTTGAGGAT 2645 GAAGTTTTGAGGAT 2645 QY 419 TyrSerThrGlyLys 131 ATCTGCACTTTAATAGGAAA 2525 ATCTGCACTTTAATAAGAAAA 2525 euGluProGlyLeuAsnGluIle 151 :::: ::: ::: | GAAGTTTTGAGGAT 2645 QAAGTT
 | SCCTAGTAGGTTAGGATACTCTCAAACTGGAACT 1900 | SCCTAGTAGGTTAGAATACTCTCAAACTGGAACT 10 10 10 10 10 10 10 1
 | SCCTAGTAGGTTAGAATACTCTCAAACTGGAACT 10 10 10 10 10 10 10 1 | SCCTAGTAGGTTAGGATACTCTCAAACTGGAAGT 2645 | SCCTAGTAGGTTAGGATACTCTCAAACTGGAAGT 2645 | SCCTAGTAGGTTAGGATACTCTCAAACTGGAACT SANGLEU | SCCTAGTAGGTTAGGATACTCTCAAACTGGAACT SACGTAGTAGGATAGGTTAGGATTATTGGTTAGAGTT 2645 SACGTACTTATCTATAATAGGATTTTTGGCCAAATTTTCGTTAGATTATATCGAC 2585 TILL
 | SCCTAGTAGGTTAGGATACTCTCAAACTGGAACT SACQUE SACGTAGTAGGATTTTGGCCAAATTTTGGTTAGATTATATCGAC 2585 196 SACGACTTATCTATAATAGAGATTTTTGGCCAAATTTTCGTTAGATTATATCGAC 2585 116 SACGACTTATCTATAATAGAGATTTTTGGCCAAATTTTCGTTAGATTATATCGAC 2585 118 SACGACCTATATCTATAATAGAGAATTTTTGGTCAACTTATATATCGAC 2585 118 ACGACCTAGATATTTTCACCCGACCTATATATAGAGCAGA 2585 118 SACGTACAAATTTTTCATCTCGCCACCTTTAAAAAGACGAGAA 2525 118 SACGTACAAATTTTTTCATCTTCATCTCGCCCCACTTTAAAAAGACGAAA 2525 118 SACGTACAAAATTTTTTTATTTATATATAAAAGATTTA 2495 118 SACGTACAAAATTTTATTTATATATAAAAGATTAA 2525 118 SACGTACAAAATTTTATTTATATATAAAAGATTAA 2525 118 SACGTACAAAATTTTATTTAAAAAAAAAAAAAAAAAAAAA | SCCROTAGGTTAGGATACTCTCAAACTGGAAGT 2645 | SCCRETARGETTAGATACTCCAAACTCCAAACTCCAAACTCCAAACTCCAAACTCCAAACTCCAAACTCCAAACTCCAAACTCCAAACTCCAAACTTCTCGTTAGACGCT 2645 Fill F | SCCPACTAGGTTAGGATACTCCCAAACTCCCAAACTCCTCAAACTCCTCAAACTCCTC
 | SCCRETAGGATRGCTCTCAAACTGGAAGT 2645 | SCCINGTANGGTTNGAATACTCTCNAACTGGAAGT 2645 | SCENEGRANGETTNGGARTACTCTCÀAACTGGAAGT 2645 FEATGLEU | SCCTAGTAAGGTTAGGATGTCTCTAAACTGGAAGT |
| TAGAATACTCTCAAACTGGAAGT | TAGAATACTCTCAAACTGGAAGTTTTGAGGAT 2645 Qy 419 | Qy 419 | ATACTACTCTCAAACTGGAAGT

 | ATAGMATACTCTCAAACTGGAAGT | WASATRCTCTCAAACTGGAAGT | WASATACTCTCAAACTGGAAGT | ATAGRATECTCTAAACTGGAAGT
 | ATAATACTCTCAAACTGGAAGTTTTGAGGAT 2645 | WAGARIACTCTCAAACTGGAAGT | 186AATACTCTCAAACTGGAAGT | TAGAATACTCTCAAACTGGAAGT | ATAATACTCTCAAACTGGAAGT
 | ATAATACTCTCAAACTGGAAGTTrTGAGGAT 2645 | ###################################### | GAAGT | GAAGT
 | GAAGT | GAAGT | GAAGTTTTGAGGAT 2645 | GAAGT
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 | GAAGTTTTGAGGAT 2645 | GAAGT
 | SACIAGITANANGTITANANGTCTCCAAACTGGAAGT | SACIALDINAMOTITALAMINGTECTOCAMACTIGAMAGT
 | SACIAGNIAMOSTIAGAMACTICICAMACTIGAMAGT | SACIAGITACANISTINGANACTICCANACTIGANGT | SACIAGITANAGTITAGANAGTCTCCAAACTIGAAGAT 2645 | SACIALD | SACIALD
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| Qy 419 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: TATGAGACTATTTCATCTGCACTTTAATAAAGAAA 2525 TTOGInGluCysLeuLeuGluProGlyLeuAsnGluIle 151 ::: ::: ::: ::: ::: | Qy 419 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: TTAATGACGACTATTTTCATCTGCACTTTAATAAAGAAA 2525 TTOGlnGluCysLeuLeuGluProGlyLeuAsnGluIle 151 ::: ::: TTATTTATAGAATTA 2495 YrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu 171 Qy 467 | Qy 419 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 :: :: :: :: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 :::

 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThr11eTyrSerThrGlyLys 131 ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 : : | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: :::
 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThr11eTyrSerThrGlyLys 131 ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 Db 1888 ATAATAGAGATTTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 Db 1888 ATAATAGAGATTTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 Db 1888 ATAATAGAGATTTTTGGCCAAATTTTCGTTAGATTATATCGAG 2585 Oy 427 I ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 : : | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThr1leTyrSerThrGlyLys 131 ::: ::: ::: ::: :::
 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrmetSerThrIleTyrSerThrGlyLys 131 :: TATGACGGACTATTTCATCTGCACTTAATAAAAGAGAA 2525 TTATGACGGACTATTTTCATCTGCACTTTAATAAAGAGAA 2525 TTOGLIGLUCYSLeuLeuLeuGluProGlyLeuAsnGluIle 151 :: TATTTATATAA | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 : : | | Qy 419 AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131
 | AAATTTCGTTAGATTATATCGAG 2585 AAAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131TyrSerThrGlyLys 131 | AAATTTCGTTAGATTATATCGAG 2585 AAATTTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ::::: ::: | Qy 419 | AAATTTCGTTAGATTATATCGAG 2585 AAAATTTCGTTAGATTATATCGAG 2585 AAAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131TyrSerThrGlyLys 131
 | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 :::::: | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 | AAATTTCGTTAGATTATATCGAG 2585 AAAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ::::: ::: ::: ::: | AAATTTCGTTAGATTATATCGAG 2585 AAAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131

 | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ::::: ::: | Qy 419
 | SATGLEU | SATISLEU
 | SACAGCTARCTANATAGAGATTTTGGCCAAATTTCGTTAATATATATCAAG 2585 CACAACTTATCATATATAGAGATTTTTGGCCAAATTTTCGTTAATATATAT | 1984 116 | SARTGLEU | |
 | SACAGCTARCTANATAGAGACTATTTCGCCAAATTTCGTTAAATAATATATACAGA | SARACTANICTATATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ACCACCTAATCATATATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ACCACCTAACTATATAGAGAAATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ACCTACTAACTATATAGAGCGACTATTTTCATCTGCCACTTTAAATAAA | SARTGLEU |
 | 1848_ 1875_ 1 | | SACHGIEU |
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| Tradfaccontinuous Trad | TATATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 | | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585

 | ### ATAATAGAGATTTTGGCCAAATTTCGTTACATTATATCGAG 2585 ################################## | ### ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATTCGAG 2585 #### ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATTCGAG 2585 ################################## | ATGGTAGTCGCCGGAATTTTGGTGAATCTATTGAAACGTTA 2435 ATGGTAGTGCCCGAATTTTGGTGATAAACGTTA 2435 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrwetSerThrileTyrSerThrGlyLys 131
 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGAGTATTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAGACGACTATTTTCATCTGCACTTTAATAAAGGAGAA 2525 TOGINGluCysLeuLeuGluProGlyLeuAsnGluIle 151 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTTGGCCAAATTTCGTTAGATAAATGAGAGA 2585 ATATGACGGACTATTTTCATCTGCACTTTAATAAAGGAGAA 2525 TOGINGLUCYSLEULEUGLUPTOGIYLEUAASNGLUILE 151 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTTGGCCAAATTTTCGTTAGATTATATCGAG 2585 ATAGTGACGGACTATTTTCATCTGCACTTTAATAAAGGAGAA 2525 TOGLIGLUCYSLeuLeuLeuGluProGlyLeuAsnGluIle 151 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrwetSerThrileTyrSerThrGlyLys 131 ::::::::: :::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrwetSerThrileTyrSerThrGlyLys 131 ::: ::: :::
 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGACTATTTCATCTGCACTTTAATAAAGGAGAA 2525 ATATGACGACTATTTTCATCTGCACTTTAATAAAGGAGAA 2525 TOGINGluCysLeuLeuGluProGlyLeuAsnGluIle 151 | | |
 | AAATTTCGTTAGATTATATCGAG 2585 AAAATTTCGTTAGATTATATCGAG 2585 AAAATTTCGTTAGATTATATCGAG 2585 TyrserThrGlyLys 131 ::: ::: ::: | | | AAATTTCGTTAGATTATACGAG 2585 AAATTTCGTTAGATTATACGAG 2585 TyrserThrGlyLys 131TyrserThrGlyLys 131TyrserThrGlyLys 131
 | AAAATTTCGTTAGATTATATCGAG 2585 AAAATTTCGTTAGATTATATCGAG 2585 AAAATTTCGTTAGATTATATCGAG 2585 ATCTGCACTTTAATAAAGGAGAA 2525 euGluProGlyLeuAsnGluTle 151 :: TAGAATTA 2495 LaTrpGluSerTrpArgSerGlu 171 | |

 | AAATTTCGTTAGATTATATCGAG 2585 AAAATTTCGTTAGATTATATCGAG 2585 AAAATTTCGTTAGATTATATCGAG 2585 ATCTGCACTTTAATAAAGGAGAA 2525 EUGLUPTOGLYLEUAATAAAGGAGAA 2525 EUGLUPTOGLYLEUAATAAAGGTTA 2495 TAAGAATTA 2495 TATTPGGLUSETTPATGSAACGTTA 2435 TTGGTGAATCTATGAAACGTTA 2435 TTGGTGAATCTATGAAAGATTGA 2378 QY 467 AAAATTTCGTTAGAAGATTGA 2378 QY 486 TYTGLUGLUTYT 183 GAGCAATCTCGTTAGAAGATGGA 2378 QY 486 | AAATTTCGTTAGATTATACGAG 2585 AAATTTCGTTAGATTATACGAG 2585 AAATTTCGTTAGATTATACGAG 2585 TyrSerThrGlyLys 131 |
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| ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: | Db 1888 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 Db 1888 ATAATAGAGATTTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 Dy 427 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 Dy 427 ATAATGACGGACTATTTTCATCTGCACTTTAATAAAGAAA 2525 Db 1828 TTAATGACGGACTATTTTCATCTGCACTTTAATAAAGAAA 2525 Db 1828 TTAATGACGGACTATTTTCATCTGCACTTTAATAAAGAAA 2525 Db 1795 TTAATGACGACTATTTATATAGAATTA 2495 YASATGLUĀTGLUĀTTTATĀ | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrmetSerThr11eTyrSerThrGlyLys 131 :: :: TATGACGGACTATTTCATCTGCACTTTAATAAAGGAGAA 2525 roglnGluCysLeuLeuLeuGluProGlyLeuAsnGluIle 151 TATTTATAGAATTA 2495 :: | Db 1888 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 Db 1888 Cy 427

 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrwetSerThrIleTyrSerThrGlyLys 131 ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: :::
 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: :: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrmetSerThr11eTyrSerThrGlyLys 131 ::: ::: ::: ::: ::
 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 : : | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ::::: ::: | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 Oy 427TyrSerThrGlyLys 131 ::::::::::::::::::::::::::::::::::: | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131
 | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGAGAAA 2525 ATCTGCACTTTAATAAAGAGAAA 2525 euGluProGlyLeuAsnGluIle 151 :: :: :: | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 :::::: ::: ::: | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 :::::: :::
 | AAATTTCGTTAGATTATATCGAG 2585 AAATTTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 :::::::::::::::::::::::::::::::::: | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TyrSeIThrGlyLys 131 ATCTGCACTTTAATAAAGAAAA 2525 euGluProGlyLeuAsnGluIle 151 ::GAATTA 2495 TAGAATTA 2495 TA

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 | 10 10 10 10 10 10 10 10 | 10 10 10 10 10 10 10 10
 | 10 10 10 10 10 10 10 10 | 10 10 10 10 10 10 10 10 | ACACCTIATCTATAATAGAGATTTTGGCCAAATTTCGTTAGATTAATAGGAG 2585 Db 1888 | ACACCTTATCTATATAGAGATTTTGGCCAAATTTCGTTAGATTAATAGGAG 2585 | DESCRIPTIATION DESCRIPTING DESCRIPTION |
 | Decirio Deci | ACACCITATCINTATATAGACATTITGGCCAAATTTCGTTACATTAATGAC 2585 | 10 10 10 10 10 10 10 10 | NCANCTIATCIANTANATAGAGATTITGGCCAAATTTATATCGAC 2585
2585 258 | 10 10 10 10 10 10 10 10 | DESCRIPTIANCTATAATAGAGATTTGGCCAAATTTGGTTAGATTATTGGAG SACACCTTATATTTGGCCAAATTTGGTTAGATTATTGGAG SACACTTATATTTGGCCAAATTTGGTTAGATTATTGGAG SACACTATTATTGGCGAAATTTTGGTTAGATATTGGAG SACACTATTATAGAGAGAATTTTGGTTAGATAAAGGAGAA SACACTATTATATTGAGCGACTATTTTCATTGGCACTTTAATAAAGGAGAA SACACTATTATTGAGCGACTATTTTCATTGCACCTTTAATAAAGGAGAA SACACTATTATGGTAGATTTTGATTGGTGAATTTTGATTGGAATTTAGAGAGAA SACACTAGAATTATTGGTAGATTTTGGTGGAATTTTGGTGAATTGAAACGTTA SACACGCCGAAAATTATTGGTAGATTTTGGTGGAATCTATTGAAACGTTA SACACGCTCGGACTATTGGATATTGGTGAATCTATTGAAACGTTA SACACGCTCGGACTATTGGATATTGGTAGAATCTAATTGAAACGTTA SACACGCTCGGACTATTGGATTATTGATTAGAAACGTTA SACACGCTCGGACTATTGGATTATTGATTTGATTAGAAACGTTA SACACGCTCGGACTATTGGATTATTGATTAGAAACGTTA SACACGCTCGGACTATTGGATTATTGATTAGAAACGTTATTTTTATTTGG SACAAATTGGTTATAATTGAAAACCAATTTTTTATTTTAGTAGAATTTTTTTT |
| ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 | ATAATAGAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThr11eTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTACATTATATCGAG 2585 hrWetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTACAGTTATATCGAG 2585 ATAATAGAGAGATTTTGGCCAAATTTTCGTTACAGTTATATCGAG 2585 ATAATAGAGAGATTTTTGGCCAAATTTTCGTTACGTTA

 | Db | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrwetSerThrIleTyrSerThrGlyLys 131 | ### ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ################################## | ATAATAGAGATTTTGGCCAAATTTCGTTACATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
 | ATAATAGAGATTTTGGCCAAATTTCGTTACATTATATCGAG 2585 hrWetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGAGATTTTGGCCAAATTTTCGTTAGATTATATCGAG 2585 ATAGACGGACTATTTTCATCTGCACTTTAATAAAGGAGAA 2525 TTAGGACGACTATTTTCATCTGCACTTTAATAAAGGAGAA 2525 TOGINGluCysLeuLeuGluProGlyLeuAsnGluIle 151 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGAGTTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGAGATTTTGGCCAAATTTTCGTTAGATTATATCGAG 2585 ATAGACGGACTATTTTCATCTGCACCTTTAATAAAGGAGAA 2525 PTATGACGGACTATTTTCATCTGCACCTTTAATAAAGGAGAA 2525 PTATGACGGACTATTTTCATCGCACCTTTAATAAAGGAGAA 2525 PTATGACGGACTATTTTATAAGAATTA 2495 PTATGACGGACTATTTTATAA | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrWetSerThrIleTyrSerThrGlyLys 131 ::: :: :::
 ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrWetSerThrIleTyrSerThrGlyLys 131 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrwetSerThrileTyrSerThrGlyLys 131 ::: | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 ATCTGCACCTTTAATATAGAGAAA 2525 EUGLUPTOGLYLEUAANGLUILE 151 :: : : : | AAATTTCGTTAGATTATATGGAG 2585 AAATTTCGTTAGATTATATGGAG 2585 OY 427TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGAAAA 2525 euGluProGlyLeuAsnGluIle 151 :: TAGAATTA 2495
laTrpGluSerTrpArgSerGlu 171 TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 GYGluAspTyrGlyAspTyrTrp 203 :: GAGCAATCTCGTTAGAAGATGGA 2378 OY 506 1717 | AAATTTCGTTAGATTATATGGAG 2585 AAATTTCGTTAGATTATATGGAG 2585 ATCTGCACTTTAATAAAGGAGAA 2525 EUGLUPTOGLYLEUASHGLUILE 151 ETAGAATTA 2495 LATTPGLUSETTPATGAAACGTTA 2495 LATTPGLUSETTPATGAAACGTTA 2435 TTGGTGAATCTATGAAACGTTA 2435 GAGCAATCTCGAAGATGGA 2378 YGLUASPTYTGLYASPTYTTGG 2324 LATTTCTAAAAGGATTTATTTGG 2324 DD 1735 | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 Oy 427TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGGAGAA 2525 EUGLUPTOGLYLEUAAAGGATA 2525 EUGLUPTOGLYLEUAAAGATTA 2495 TAAGAATTA 2495 TATTPGLUSETTPATGSAACGTTA 2495 TTGGTGAATCTATGAAACGTTA 2435 TTGGTGAATCTATGAAACGTTA 2435 TTGGTGAATCTATGAAAGATTG 2378 QY 486TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATTGA 2378 QY 486 | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGAAAA 2525 euGluProGlyLeuAsnGluIle 151 ::GAATTA 2495 1aTrpGluSerTrpArgSerGlu 171 1 | AAATTTCGTTAGATTATATGGAG 2585 AAATTTCGTTAGATTATATGGAG 2585 ATCTGCACTTTATATATATGGAGAA 2525 ATCTGCACTTTAATAAAGGAAA 2525 euGluProGlyLeuAsnGluIle 151 :: ::: Db 1795 TAGAATTA 2495 141719GluSerTrpArgSerGlu 171 1716GTGAARCTATGAAACGTTA 2435 TTGGTGAARCTATGAAACGTTA 2435 TTGGTGAARCTATGAAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: GAGCAATCTCAAAGGATTAATTTGG 2324 Oy 526 Oy 526
 | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 ATCTGCACCTTTAATATAGAGAAA 2525 ATCTGCACCTTTAATAAAAGAAA 2525 EUGLUPFOGLYLEUAARGLUILE 151 :: ::: ::: ::: ::: | AAATTTCGTTAGATTATATGGAG 2585 AAAATTTCGTTAGATTATATGGAG 2585 OY 427TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGAAAA 2525 euGluProGlyLeuAsnGluIle 151 :: TARGAATTA 2495 LaTrpGluSerTrpArgSerGlu 171 | AAATTTCGTTAGATTATATGGAG 2585 AAATTTCGTTAGATTATATGGAG 2585 ATCTGCACTTTAATAAAGGAGAA 2525 ATCTGCACTTTAATAAAAGAAAA 2525 EUGLUPTOGLYLEUASNGLUILE 151 ETATGAATTA 2495 TATTPGLUSETTPATGAAACGTTA 2495 TATTPGLUSETTPATGAAACGTTA 2435 TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTATTAAAAGAATGGA 2378 GAGCAATCTCGTTAGAAAGATGGA 2378 YGLUASPTYTGLYASPTYTTP 203 ETATTCTCAAAGATTATTTGG 2324 ALASP | AAATTTCGTTAGATTATATGGAG 2585 AAATTTCGTTAGATTATATGGAG 2585 ATCTGCACCTTTAATATAGAGAAA 2525 EUGLUPTOGLYLEUAAAGGAGAA 2525 PA

 | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 TyrSerThrGlyLys 131 TyrSerThrGlyLys 131 | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 ATCTGCACCTTTAATATATACGAG 2585 ATCTGCACCTTTAATAAAAGGAGAA 2525 EUGLUPTOGLYLEUASNGLUILE 151 ::
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| ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATAGAG 2585 ATAATAGAGATTTTTGGCCAAATTTTGGTyLys 131 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGAG 2585 hrMetSerThrileTyrSerThrGlyLys 131

 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGAG 2585 ATAGTAGAGGACTATTTTCATCTGCACTTTAATAAAGGAAA 2525 ATATGACGGACTATTTTCATCTGCACTTTAATAAAGGAAA 2525 ATAGTAGACGGACTATTTTATAAGAATTA 2495 TTATTATAGAATTA 2495 TTATTTATAGAATTA 2495 ATAGTAGTCGCTGGTATTTGGTGAATCTATTGAAACGTTA 2435 ATAGTAGTCGCTGGTATTTTGGTGAATCTATTGAAACGTTA 2435 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGAG 2585 ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGAG 2585 ATAGTAGAGGACTATTTTCATCTGCACTTTAATAAAGAAA 2525 TTATGACGGACTATTTTCATCTGCACTTTAATAAAGAAA 2525 TTATGACGGACTATTTTCATCTGCACTTTAATAAAGAAA 2525 TTATGACGGACTATTTTCATCTGCACTTTAATAAAGAAA 2525 ATAGTAGTAGTCATTTATTATA
 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrwetSerThrileTyrSerThrGlyLys 131 ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGG 2585 hrMetSerThrileTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrwetSerThrileTyrSerThrGlyLys 131 :::
 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGGG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATAGG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: ::: ::: ::: | AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGGAGAA 2525 ATCTGCACTTTAATAAAGGAGAA 2525 euGluProGlyLeuAsnGluIle 151 :: | AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGAGAAA 2525 ATCTGCACTTTAATAAAGAGAAA 2525 euGluProGlyLeuAsnGluIle 151 :: ::
 | AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ::::: ::: ::: ATCTGCACTTTAATAAAGGAGAA 2525 euGluProGlyLeuAsnGluIle 151 :: ::: ::: TAGAATTA 2495 TAGAATTA 2495 TATTTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTATTGAAACGTTA 2435 | AAATTTCGTTAGATTATATCGAG 2585 AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGGAGAA 2525 ATCTGCACTTTAATAAAGGAGAA 2525 euGluProGlyLeuAsnGluIle 151 :: | AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGAAA 2525 ATCTGCACTTTAATAAAGAAA 2525 ATCTGCACTTTAATAAAGAAA 2525 ATCTGCACTTTAATAAAGAAA 2525 ATTAGAATTA 2495 TAAGAATTA 2495 TAAGAATTA 2495 TAAGAATTA 2495 TAA | AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ::::: ::: ::: ATCTGCACTTTAATAAAGGAGAA 2525 euGluProGlyLeuAsnGluIle 151 :: ::: ::: TAGAATTA 2495 TATTPGIUSerTrpArgSerGlu 171 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::
 | AAATTTCGTTAGATTATACGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGGAGAA 2525 ATCTGCACTTTAATAAAGGAGAA 2525 euGluProGlyLeuAsnGluIle 151 :: :: | AAATTTCGTTAGATTATACGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGAAAA 2525 ATCTGCACTTTAATAAAGAAAA 2525 ATCTGCACTTTAATAAAGAAAA 2525 euGluProGlyLeuAsnGluIle 151 :: :: | AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131TyrSerThrGlyLys 131 DD 1828 ATCTGCACTTTAATAAAGGAGAA 2525 euGluProGlyLeuAsnGluIle 151 :GAATTA 2495 TAAGAATTA 2495 TATTPGGluSerTrpArgSerGlu 171 | AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 DD 1828 ATCTGCACTTTAATAAAGGAGAA 2525 euGluProGlyLeuAsnGluIle 151 :: ::

 | AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGAAA 2525 ATCTGCACTTTAATAAAGAAA 2525 euGluProGlyLeuAsnGluIle 151 :: :: 2495 TAGAATTA 2495 TAGAATTA 2495 TATyrGluSerTlpArgSerGlu 171 :: | AAATTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGGAGAA 2525 euGluProGlyLeuAsnGluIle 151 ::GAATTA 2495 TA
 | CAAACTTATCTATATATAGAGATTTTGGTCAAATTTTCGTTAGATTATATAGAG 2585 CAAACTTATCTATATATAGAGATTTTGGTCAAATTTTCGTTAGATTATAGAG 2585 CI | COAAACTTATCTATATATAGAGATTTTGGTCATAGATTATATAGGAG 2585 CIT
 | CAAACTTATCTATATATAGAGATTTTGGTCAAATTTTCGTTTAGATTATATCGAG 2585 | PACAACTTATCTATATATAGAGATTTTGGTCAAATTTTCGTTAGATTATATGGAG 2585 TILLELEUASSTThrMetSerThrIleTyrSerThrGlyLys 131 | CAAACTTATCTMAATAGAGATTTTGGTCAAATTTTCGTTAGATTATATCGAG 2585 | CAAACTTATCTATATATAGAGATTTTGGTCAAATTTAGATTATATGGAG 2585 Carle C | CAAACTTATCTATATATAGAGATTTTGGTCAAATTTTCGTTAGATTATATCGAG 2585 CI | CAAACTTATCTATATATAGAGATTTTGGTCAAATTTTGGTTAGATTATATGGAG 2585 FileLeuasnThrhetesrThrile
 | CACACCTTATATATATAGAGATTTTGGCCAAATTTTGGTTAGATTATATCGGC 2585 CACACCTTATATATATAGAGA 2585 CACACCTTATATATATATATAGAGAGAGAGAGAGATTTTTGGCCAAATTTTCATCTTAGAGATTATATATA | CAAACTTATATATATAGAGATTTTGGCCAAATTTTGGTTAGATTATATCGGC 2585 | CACACCTTATATATATAGAGATTTTGGCCAAATTTTGGTTAGATTATATCGGC 2585 CACGACACTTTTTCGCCAAATTTTCGTTAGATTATATATCGGC 2585 CACGACACTTTTTCATCTGGCCACTTTTTTCATCTGGCCACTTTTTTTT
 | CAAACTTTTTGGCCAAATTTTGGCCAAATTTTGGTTAGATTATATCGGC 2585 | CACACCTTATATATAGAGATTTTGGCCAAATTTTGGTTAGATTATATCGGC 2585 | CAAACTTTTTGGCCAAATTTTGGTAGATTATATATGGG 2585 | CAAACTTATCTATATAGAGATTTTGGCCAAATTTTGGTTAGATTATCGAG 2585 PILLEUASSTThrWetSerThrIle |
| ATAATAGAGATTTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTTGGCCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTTGGCCCAAATTTTGGTLYS 131 III ::: | ATAATAGAGATTTTTGGCCAAATTTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTTGGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: | ATAATAGAGATTTTTGGCCAAATTTTGATTTATATCGAG 2585

 | ATAATAGAGATTTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrmetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTGGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 ATAATAGAGATTTTTGGCCAAATTTTCGTTAATAAAAGAGAA 2525 ATAATGACGGACTATTTTCATCTGCACTTTAATAAAGAGAA 2525 ATAATGACGGACTATTTTCATCTGCACTTTAATAAAGAGAA 2525 ATAATGACGAATTTATATAAGAATTA 2495 ATAGATAGTAGTCGTATTTTGGTGAAATCTATTGAAACGTTA 2435 ATGGTAGTCGCTGGTATTTTGGTGAAATCTATTGAAAACGTTA 2435 Qy 486 | ATAAHAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585
 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 :: | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: ::: ::: | ATAATTAGAGATTTTTGGCCAAATTTTGGTTAGATTATATCGAG 2585 | ###################################### | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrMetSerThrIleTyrSerThrGlyLys 131 ::: :::
 | ATAATAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrmetSerThrileTyrSerThrGlyLys 131 : : | ATAATTAGAGATTTTGGCCAAATTTCGTTAGATTATATCGAG 2585 hrmetSerThrIleTyrSerThrGlyLys 131 ::: :: | AAAITTCGTTAGATTATACGAG 2585 TyrSerThrGlyLys 131 AICTGCACTTTAATAAAGAAA 2525 AICTGCACTTTAATAAAGAGAAA 2525 euGluProGlyLeuAsnGluIle 151 :GAATTA 2495 TAGAATTA 2495 1aTrpGluSerTrpArgSerGlu 171 | AAAITTCGTTAGATTATACGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGAAA 2525 ATCTGCACTTTAATAAAGAAAA 2525 ATCTGCACTTTAATAAAGAAAA 2525 ATCTGCACTTTAATAATAAAGAAAA 2525
ATCTGCACTTTAATAAAGAAAAAAAAAAAAAAAAAAAA | AAAITTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGAAAA 2525 euGluProGlyLeuAsnGluIle 151 :: | AAAITTTCGTTAGAFTATATCGAG 2585TyrSerThrGlyLys 131 ::: ::: | AAAITTCGTTAGATTATACGAG 2585TyrSerThrGlyLys 131 | AAAITTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGAAAA 2525 euGluProGlyLeuAsnGluIle 151 ::
 | AAAITTCGTTAGATTATACGAG 2585TyrSerThrGlyLys 131 ::: ::: :: | AAAITTCGTTAGATTATACGAG 2585TyrSerThrGlyLys 131 | AAAITTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 DD 1828 ATCTGCACTTTAATAAAGAAAA 2525 euGluProGlyLeuAsnGluIle 151 :: | AAAITTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGAAAA 2525 euGluProGlyLeuAsnGluIle 151 :

 | AAAITTTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGGAGAA 2525 EUGLUPTOGLYLEUASAGGAGAA 2525 PAGAATTA 2495 TATTTPGLUSETTPATGSETGLU 171 LITTTGGTGAATCTATTGAAAGGTTA 2435 TyrGluGluTyr 183 TyrGluGluTyr 183 GAGCAATCTCTGTTAGAAAGATGGA 2378 YIGGUAASPTYTGLUGLUTYT 203 III | AAAITTCGTTAGATTATATCGAG 2585 TyrSerThrGlyLys 131 ATCTGCACTTTAATAAAGAAA 2525 ATCTGCACTTTAATAAAGAGAAA 2525 ATCTGCACTTTAATAAAGAGAAA 2525 ATCACCACTTTAATAAAGAGAAA 2525 Qy 447 euGluProGlyLeuAsnGluIle 151 :: | ACARCTIFACUTATUTATURARIANS CONTINUES
 | ACACACTIANCEMANITINGGCAAANTTCGTTAGATTAMTGGAG 2885 COPACTIANCEMANITATION | ACANCTIFACURATATIVICGCCAAATTTCGTTAGATTATATICGA 2885 COGTACTAGATATATATATAGAG 2885 COGTACTAGATATATATATAGAGGACTATTTTCATTTGAGATTATATAGAG 2885 COGTACTAGATATATATAGAGGACTATTTTCATTTGACATTTAAAAGGAGAA 2525 COGCGAAAATTATTTATA | | ACARCTIANCUMARANTITICGCCAMANTITICGTTAGATATATICGAG 2285 COTACTACUMATITICGTTAGATATATICGAG 2285 COTACTACATATATACAGATATTTCATCTGCACTAGATATATICGAG 2285 COTACTACATATTATCACCGCCTTTAATATAAAGAAAA 2525 COTACTACATATTATCACCGCCTTTAATATAAAGAAAA 2525 COTACTACATATTATCACCGCCTTTAATATAAAGAAAA 2525 COTACTACATATTATCACCCCTTTAATATAAAGAAAAA 2525 COTACTACATATTATCACCCTTTAATATAAAGAAAAA 2525 COTACTACATATCACCCTTTAATATAAAGAAAAA 2525 COTACATATCACACCTCCTTAATATAAAGAAAAA 2525 COTACATATCACACCTCCTTAATATAAAGAAAAAAAAAAA
 | | ACARCTIFACULARATETITICGCCAAATTTCGTTAGATTATATGGG 2885 CGTACTRACHATTATATATGGG 2885 CGTACTRACHATATATATATGGAC 2885 CGTACTRACHATATATATATGGACTATTTATATATATGGACTAGATATATAT | | |
 | | ACANCTIFICATION ANAMATITICS 2885 |
 | | ACACATHATCH HANDARAT TITGGCCAAATTTGGTTAGTTTATTGCAG 285 ITITLECUASHTATATGAGGAATATTTGGCCAAATTTGGTTAGTTTATTAGAGAAA 255 ACGTACTAGATATTATGAGGAATATTTTCATCTGCACTTTAATAAAGAAA 2525 ACGTACTAGATATTATGAGGAATATTTTCATCTTCACTTTAATAAAGAAAA 2525 ACGTACTAGATATTATGAGGAATTTTTATTTATAATAAAGAAAA 2525 ACGCGAAAATTTATTTATAA |
| ArmetSerThrIle Qy 427 ::: ::: ::: ::: PTATGACGGACTATTTCATCTGCACTTTAATAAAGAAAA 2525 Db 1828 1828 TroGlnGluCysLeuLeuGluProGlyLeuAsnGluIle 151 ::: ::: ::: ::: TATTTTATAGAATTA 2495 Qy 467 YrAsnGluArqLeuTrpAlaTrpGluSerTrpArgSerGlu 171 | hrmetSerThrIleTyrSerThrGlyLys 131 0y 427 ::: ::: ::: 1828 TTATGACGGACTATTTCATCTGCACTTTAATAAAGGAAA 2525 0y 447 rogInGluCysLeuLeuGluProGlyLeuAsnGluIle 151 0y 447 TATTATTATAGAATTA 2495 0p 1795 yrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu 171 0p 467 | A 27 | hrmetSerThr11e Qy 427 ::: ::: ::: ::: TTATGACGGACTATTTTCATCTGCACTTTAATAAAGGAGAA 2525 Db 1828 roGlnGluCysLeuLeuGluProGlyLeuAsnGluIle 151 Qy 447 roGlnGluCysLeuLeuGluProGlyLeuAsnGluIle 151 Db 1795 TATTTATAGAATTA 2495 Qy 467 yrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu 171 Db 1780

 | A 27 A 27 | ATTOGETAGTTGTGTGTGAATCTTGTTTATTTGTTTATTTTGTTTATTTTGTTTATTTTGTTTATTTTATTTTTT | hrmetSerThrIleTyrSerThrGlyLys 131 0y 427 ::: ::: ::: 11 128 TTATGACGGACTATTTCATCTGCACTTTAATAAAGGAGAA 2525 0y 447 roclnGluCysLeuLeuGluProGlyLeuAsnGluIle 151 0y 447 rroclnGluCysLeuLeuGluProGlyLeuAsnGluIle 151 0b 1795 TATTTATAGAATTA 2495 0y 467 yrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu 171 17 0y 467 :: :: | hrmetSerThrIleTyrSerThrGlyLys 131 0y 427 H ::: | ATTOCHEU | ATGGTAGTCGCTGGTATTTTGGTGAATCTAATGAAACGTTA 2435
 | hrmetSerThrIle 9y 427 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: | ATTATGACGGACTATTTTCGTGCACTTTAATAAAGGAAA 2525 TTATGACGGACTATTTTCATCTGCACTTTAATAAAGGAAA 2525 TTATGACGGACTATTTTCATCTGCACTTTAATAAAGGAAA 2525 TTATGACGGACTATTTTCATCTGCACCTTTAATAAAGGAAA 2525 TTATGACGCACTTTTAATAAAGGAAA 2525 TTATTTATAAA | hrmetSerThrileTyrSerThrGlyLys 131 | hrmetSerThr11e 0y 427 ::: ::: | hrmetSerThrIleTyrSerThrGlyLys 131
 | Oy 427TyrSerThrGlyLys 131 Db 1828 ATCTGCACTTTAATAAAGAAA 2525 euGluProGlyLeuAsnGluIle 151 :GAATTA 2495 TAAGAATTA 2495 TATTPGluSerTrpArgSerGlu 171 | Oy 427TyrSerThrGlyLys 131 Db 1828 ATCTGCACTTTAATAAAGAAAA 2525 Colorada 2525 Db 1828 Db 1828 Db 1828 Db 1828 Db 1828 Db 1828 Db 1795 Db 1795 Db 1795 Db 1795 Db 1795 Db 1780 Db 1735 | Oy 427TyrSerThrGlyLys 131TyrSerThrGlyLys 131TyrSerThrGlyLys 131 | Oy 427TyrSerThrGlyLys 131 Db 1828 ATCTGCACTTTAATAAAGAAAA 2525 euGluProGlyLeuAsnGluIle 151 :GAATTA 2495 TAAGAATTA 2495 TAGTIGTGAATCTATGAAACGTTA 2435 TTGGTGAATCTATGAAACGTTA 2435 TTGGTGAATCTATTAGAAGATGGA 2378 Qy 486TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 TTGGTGAAGGATTTAGTTTGG 2324 | Oy 427TyrSerThrGlyLys 131 Db 1828 ATCTGCACTTTAATAAAGAAA 2525 euGluProGlyLeuAsnGluIle 151 :: ::
 | Oy 427TyrSerThrGlyLys 131TyrSerThrGlyLys 131TyrSerThrGlyLys 131 | Oy 427TyrSerThrGlyLys 131 Db 1828 ATCTGCACTTTAATAAAGAAA 2525 euGluProGlyLeuAsnGluIle 151 :GAATTA 2495 TAAGAATTA 2495 TAA | Oy 427TyrSerThrGlyLys 131 Db 1828 ATCTGCACTTTAATAAAGAAA 2525 euGluProGlyLeuAsnGluIle 151 :: :: | Oy 427TyrSerThrGlyLys 131TyrSerThrGlyLys 131TyrSerThrGlyLys 131
 | Oy 427TyrSerThrGlyLys 131TyrSerThrGlyLys 131 Db 1828 ATCTGCACTTTAATAAAGGAAA 2525 euGluProGlyLeuAsnGluIle 151 :: :: : :: :

 | Oy 427TyrSerThrGlyLys 131 Db 1828 ATCTGCACTTTAATAAAGAAAA 2525 euGluProGlyLeuAsnGluIle 151 : | Oy 427TyrSerThrGlyLys 131 Db 1828 ATCTGCACTTTAATAAAGAAA 2525 euGluProGlyLeuAsnGluIle 151 :GAATTA 2495 TAAGAATTA 2495 TAA | | |
 | | YELLEUBASDThrMetSeTThrIle | |
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 | III | |
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 | hrMetSerThrIleTyrSerThrGlyLys 131 ::: ::: ::: ::: ::: | hrMetSerThrileTyrSerThrGlyLys 131 0y 427 ::: ::: ::: ::: ::: ::: ::: ::: rogInGluCysLeuLeuGluProGlyLeuAsnGluIle 151 0y 447 rogInGluCysLeuLeuGluProGlyLeuAsnGluIle 151 0y 447 ::: ::: ::: ::: ::: 0p 1795 | hrMetSerThrIle 0y 427 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: 0y 447 roGlnGluCysLeuLeuLeuGluProGlyLeuAsnGluIle 151 0y 447 rroGlnGluCysLeuLeuGluProGlyLeuAsnGluIle 151 0y 447 ::: ::: ::: 0y 447 | hrMetSerThr11e Oy 427 ::: :::::::: ::: Db 1828 TTATGACGGACTATTTTCATCTGCACTTTAATAAAGGAGAA 2525 Db 1828 TroGlnGluCysLeuLeuLeuGluProGlyLeuAsnGluIle 151 Oy 447 roGlnGluCysLeuLeuLeuGluProGlyLeuAsnGluIle 151 Db 1795 TTATTTATA
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 | ### STPPOASPASPTOGLIGUCYSLEULEUGIUPFOGLYLEUASDCIUILE 151 | ### SPPTOASPASPTOGLIGLUCYSLEULEUGULPTOGLYLEUASNGCLUILE 151 | ### SPPTOASPASHPTOGLIGLUCYSLEULEUGULPTOGLYLEUASHCUITLE 151 | ### SPPTOASPASPTOGLIGLUCYSLEULEUGUPTOGLYLEUASRGLUILE 151
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 | YRASHGLUArgLeuTrpAlaTrpGluSerTrpArgSerGlu 171 | YRASNGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu 171 | yrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu 171 | YrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu 171 Db 1780 ATGGTAGTCGCTGGTATTTTGGTGAATCTATTGAAACGTTA 2435 Qy 486
 | YRASDGLUARGLEUTEPALATEPGLUSETTEPALGSERGLU 171 | yrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu 171 | yrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu 171 | YRASHGLUARGLEUTRPALATROGUSETTRPATGSERGLU 171 | Qy 467 YrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu 171
 | YRASHGLUARGLEUTRPALATREGLUSETTRARGSERGLU 171 QY 467 ::: ::: Db 1780 ATGGTAGTCGCTGGTATTTTGGTGAAATCTATTGAAACGTTA 2435 Db 1780 roleuTyrGluGluTyr 183 QY 486 ::: Db 1735 CTCTGGATAAGGCAATCTCGTTAGAAGATGGA 2378 Db 1735 CTCTGGATAAGGCAATCTCGTTAGAAGATGGA 2378 QY 506 etalaargalaasnHisTyrGluAspTyrGlyAspTyrTrp 203 QY 506 | yrAsnGluArgLeuTrpAlaTrpGluSerTrpArgSerGlu 171 | AGRICAL AGRI | laTrpGluSerTrpArgSerGlu 171 TTGGTGAARCTATGAAACGTTA 2435 TTGGTGAARCTATGAAACGTTA 2435 TGGTGAARCTATGAAACGTTA 2435 Qy 486 TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: | A
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 | ATTPGluSerTrpArgSerGlu 171 Qy 467 | ATTPGIUSETTPATSSETGIU 171 | ATTPGLUSETTPARGSETGLU 171 | ATTPGluSerTrpArgSerGlu 171 Qy 467 Control Qy 467 Qy 467 Qy 467 Qy 467 Qy 467 Qy 467 Qy 486 Qy 506 | ATTPGIUSETTPATGSETGIU 171
 | laTrpGluSerTrpArgSerGlu 171 Qy 467 Cy 1780 Cy 17 | ATTPGluSerTrpArgSerGlu 171 Qy 467 | ATTPGluSerTrpArgSerGlu 171

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 | 1aTrpGluSerTrpArgSerGlu 171 | IaTrpGluSerTrpArgSerGlu 171 | 1aTrpGluSerTrpArgSerGlu 171 | InTrpGluSerTrpArgSerGlu 171
 | ATTPGLUSETTIPATGSETGLU 171 | IaTrpGluSerTrpArgSerGlu 171 | |

 | 1aTrpGluSerTrpArgSerGlu 171 | IaTrpGluSerTrpArgSerGlu 171
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 | | | | | ### SINSETLEUASPTYPASNGLUARGLEUTPPALATEPGLUSETTEPARGSERGLU 171
 | ### SISETLEUASPTYPASNGLUARGLEUTPPALATTPGLUSETTIPARGSERGLU 171 | | ### SINSETLEUASPTYPASNGLUARGLEUTPPALATEPPALGSERGLU 171 | ### SISSETLEUASPTYRASGCLUATGLEUTTPALATTPGLUSETTYPATGSETGLU 171
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 | Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | YTGLUASPTYTGLYASPTYTTP 203 ::: Db 1717GATTCTCAAGGATTTATTTGG 2324 alasp | Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | QY 506 YIGHUASPTYRGIAASPTYRTIP 203 GATTCTCAAAGGATTTATTTGG 2324 ALASP

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 | YTGluAspTyrGlyAspTyrTrp 203 ::: | yrGluAspTyrGlyAspTyrTrp 203 ::: | yrGluAspTyrGlyAspTyrTrp 203 :::GATTCTCAAGGATTTATTTGG 2324 Ov 526 | yrGluAspTyrGlyAspTyrTrp 203 :::
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 | p 203 | p 203 | yrGluAspTyrGlyAspTyrTrp 203 | yrGluAspTyrGlyAspTyrTrp 203
 | yrGluAspTyrGlyAspTyrTrp 203 ::: Db 1717GATTCTCAAGGATTTATTTGG 2324 | yrGluAspTyrGlyAspTyrTrp 203::: | YTG1UASPTYTG1YASPTYTTP 203 ::: Db 1717 GATTCTCAAGGATTTATTTGG 2324 OV 526 | yrGluAspTyrGlyAspTyrTrp 203 -:::
 | yrGluAspTyrGlyAspTyrTrp 203 ::: GATTCTCAAGGATTTATTTGG 2324 alAsp | yrGluAspTyrGlyAspTyrTrp 203 ::: GATTCTCAAGGATTTATTTGG 2324 alAsp | yrGluAspTyrGlyAspTyrTrp 203 ::: GATTCTCAAGGATTATTTGG 2324 alAsp | yrGluAspTyrGlyAspTyrTrp 203 :::

 | yrGluAspTyrGlyAspTyrTrp 203 ::: GATTCTCAAGGATTTATTTGG 2324 alAsp | yrGluAspTyrGlyAspTyrTrp 203 1 ::: GATTCTCAAGGATTTATTTGG 2324 Db 1717 alAsp 213 Qy 526 alAsp 213 Db 1693
 | 2uLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrTrp 203 ::: ::: :: :: :: :: :: :: :: :: :: :: :: ::: :::: :::::: :::::::::::::::::::::::::::::::::::: | 2uLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrTrp 203 ::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::: ::: ::: ::: ::: :::: :::: ::::: :::::: ::::::::::::::::::::::::::::::::::::
 | 20LLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrTrp 203 ::: :: :: :: :: :: :: :: :: :: :: ::: :::: :::::::::: :::::::::::::::::::::::::::::::::::: | PullysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrp 203 :: :: | 20LLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrTrp 203 ::: ::: 20CGAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTATTGG 2324 Db 1717 30CGAAATGGTATAGCCTTATTGGATGLUVALASnGLYVALASpT | 20LLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrp 203 ::: 100 111 | 20LLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrTrp 203 ::: :: :: :: :: :: :: :: :: :: :: :: :::: ::: ::: :::
 | 20LLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrp 203 ::: 203 ::: ::: :: 3CCGAAATGGTATTGGATGLUVALASD | 20LLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrTrp 203 ::: ::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::: ::: ::: ::: ::: ::: :::: :::: ::::: :::::: :::::::::::::::::::::::::::::::::::: | 20LLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrTrp 203 ::: ::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::: ::: :::: ::::: :::::: ::::::::::: :::::::::::::::::::::::::::::::::::: | 20LLysAsnGlumetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrp 203 20.:: ::: 30CGAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTATTTG 2324 20.5 2324 20.5 2324 20.5 2324 20.7 2324 20.7 2324 20.7 2324 20.7 2324 20.7 2264 20.7 2264 20.7 2264 20.7 2264 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 20.7 22.7 </td <td>PULYSANGLUMETALAAGALAASHHISTYTGLUASPTYTTIP 203 ::: 203 ::: ::: ::: GCGAAATGGTTATTGGATTGATTCTCAAGGATTTATTTGG 2324 Db 1717 GGGLYASPTYT</td> <td>20LLysAsnGlumetAlaArgAlaAsnHisTyrGluAspTyrTyp 203 ::: 203 ::: ::: ::: 3CGAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTATTGG 2324 Db 1717 3CGAAATGGTATAGCCTTATTGGAT</td> <td>20LLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrp 203 20.::: ::: 30CGAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTTATTTGG 2324 30CGAAATGGTATAGCCTTATTGGAT</td> <td>PuLysAsnGlumetAlaArgAlaAsnHisTyrGluAspTyrTyp 203 ::: ::: ::: </td>
 | PULYSANGLUMETALAAGALAASHHISTYTGLUASPTYTTIP 203 ::: 203 ::: ::: ::: GCGAAATGGTTATTGGATTGATTCTCAAGGATTTATTTGG 2324 Db 1717 GGGLYASPTYT | 20LLysAsnGlumetAlaArgAlaAsnHisTyrGluAspTyrTyp 203 ::: 203 ::: ::: ::: 3CGAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTATTGG 2324 Db 1717 3CGAAATGGTATAGCCTTATTGGAT | 20LLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrp 203 20.::: ::: 30CGAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTTATTTGG 2324 30CGAAATGGTATAGCCTTATTGGAT | PuLysAsnGlumetAlaArgAlaAsnHisTyrGluAspTyrTyp 203 ::: ::: :::
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 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YEGLUASPTYTG1 203 III III GATTCTCAAGGATTATTTGG 2324 alasp | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
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 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 YGLUASpTYrGlyAspTyrTrp 203 :: | GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTytTrp 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 Prolimage TyrelyaspTyrTrp 203 ::
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 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGAATGA 2378 GAGCAATCTCGTTAGAAGAATGGA 2378 9761uAspTyrGlyAspTyrTrp 203 9777GATTCTCAAGGATTAATTTGG 2324 11 | GAGCAATCTCGTTAGAAGAFGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | Db 1735 GAGCAATCTCGTTAGAAGATGGA 2378 PYGLUASPTYGLYASPTYTTP 203 :::
 | GAGCAATCTCGTTAGAAGATGA 2378 Db 1/35 YrGluAspTYrGlyAspTYrTrp 203 Qy 506 YrGluAspTYrGlyAspTYrTrp 203 Db 1717 GATTCTCAAGGATTTATTTGG 2324 Db 1717 Alasp | GAGCAATCTCGTTAGAAGATGGA 2378 YTG1UASpTYrG1YASPTYrTTP 203 | GATTCTCAAGGATTTATTTGG 2324 | | GATTCTCAAGGATTTATTTGG 2324
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 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YTG1UASpTYTG1YASpTYTTTP 203 III | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | ### DB 1735 ###################################
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 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 :::GATTCTCAAGGATTAGTTGG 2324 GATTCTCAAGGATTTAGTTGG 2324 alAsp | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YYG1UASPTYTTYP 203 ::: | ### DB 1735 ### GAGCAATCTCGTTAGAAGATGA 2378 ### QY 506 ### PART
 | GAGCAATCTCGTTAGAAGATGA 2378 Db 1/35 GAGCAATCTCGTTAGAAGATGA 2378 Qy 506 YrGluAspTyrGlyAspTyrTrp 203 Db 1717 GATTCTCAAGGATTTATTTGG 2324 Db 1717 ALASp | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YTGLUASPTYTGLYASPTYTTP 203 ::: | -::: Db 1717GATTCTCAAGGATTTATTTGG 2324 2324 24 25 26 27 27 28 29 29 29 29 29 29 29 29 20 20 | | GATTCTCAAGGATTTATTTGG 2324 alAsp 213 column 1
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| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTATTGAAACGTTA 2435 Qy 486TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: -GATTCTCAAGGATTAATTTGG 2324GATTCTCAAGGATTTATTTGG 2324 20 526 alAsp | TTGGTGAATCTATTGAAACGTTA 2435 Qy 486TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :: | Qy 486 | Qy 486

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 PrGluAspTyrGlyAspTyrTrp 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 ":" | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YTGLIASPTYTGLYASPTYTTP 203 ::: -GATTCTCAAGGATTTATTTGG 2324 -CATTCTCAAGGATTTATTTGG 2324 -CATTCTCAAGGATTTATTTGG 2324 -CATTCTCAAGGATTTATTTGG 2324 -CATTCTCAAGGATTTATTTGG 2324 -CATTCTCAAGGATTTATTTGG 2324 -CATTCTCAAGGATTTTCTTTTGCCTAT 2264 -CATTCTATTTCTTTTGCCTAT 2264 -CATTCTATTCTTTTGCCTAT 2264 -CATTCTATTTCTTTTGCCTAT 2264 -CATTCTATTTCTTTTGCCTAT 2264 -CATTCTATTTCTTTTGCCTAT 2264 -CATTCTATTTCTTTTGCCTAT 2264 -CATTCTATTTCTTTTGCCTAT 2264 -CATTCTATTCTTTTGCCTAT 2264 -CATTCTATTCTTTTGCCTAT 2264 -CATTCTATTCTTTTGCCTAT 2264 -CATTCTATTTCTTTTGCCTAT 2264 -CATTCTATTCTTTTGCCTAT 2264 -CATTCTATTTCTTTTGCCTAT 2264 -CATTCTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | | GATTCTCAAGGATTTATTTGG 2324 Db 1717 alAsp213 | GATTCTCAAGGATTTATTTGG 2324 | GATTCTCAAGGATTTATTTGG 2324
alasp213213 TTGACCTGTATTTCTTTGCCTAT 2264 algluHisThrPheGluGluIle 233 | GATTCTCAAGGATTTATTTGG 2324 | 2264 alAsp | Qy 526 :: Db 1693 TTGACCTGTATTTTTTTTTTTGCCTAT 2264 Qy 539 alGluHisThrPheGluGluIle 233 Qy 539
 | 213 | 213 Db 1693 2264 Oy 539 233 | 2264 Db 1693
2264 Qy 539 | 2264 Db 1693
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 | 233 Qy 539 | 233 Qy 539 | NTTATAGAGGAGCAAFCAGAGATTTTTACCAT
 | NTATAGAGGAGCAATCAGAATTTTTACCAT | VITATAGAGGAGCAATCAGAGATTTTTACCAT
 | NTTATAGAGGAGCAAFCAGAGATTTTTACCAT | NTTATAGAGGAGCAAFCAGAGATTTTTACCAT | ATTATAGAGGAGCAATCAGAATTTTTACCAT | NTTATAGAGGAGCAAFCAGAGATTTTTACCAT
 | NTTATAGAGGAGCAAFCAGAGATTTTTACCAT | ATTATAGAGGAGCAATCAGAATTTTTACCAT | NTTATAGAGGAGCAATCAGAGATTTTTACCAT | NTTATAGAGGAGCAAFCAGAGATTTTTACCAT
 | NTTATAGAGGAGCAATCAGAATTTTTACCAT | ATTATAGAGGAGCAATCAGAATTTTTACCAT | NTTATAGAGGAGCAATCAGAGATTTTTACCAT | NTTATAGAGGAGCAATCAGAGATTTTTACCAT
 |
| TTGGTGAAHCTATTGAAAGGTTA 2435 TTGGTGAAHCTATTGAAAGGTTA 2435 Qy 486TyrGluGluTyr 183 ::: ::: GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTxp 203 | TTGGTGAARCTATTGAAACGTTA 2435 Qy 486TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGUASPTYTTP 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::

 | TyrGluGluTyr 183 | 1735 GAGCAATCTCGTTAGAAGATGGA 2378 Db 1735 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 YTG1UASpTYrT1y 203 Qy 506 YTG1UASpTYTATTTGG 2324 Qy 526 AlAsp | GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGGA 2378 Db 1/35 YrGluAspTYrGlyAspTyrTrp 203 Qy 506 YrGluAspTYrGlyAspTyrTrp 203 Db 1717 GATTCTCAAGGATTTATTTGG 2324 Db 1717 -alAsp | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YTGLUASPTYTGLYASPTYTTP 203 SHORT CTCAAGGATTAATTTGG 2324 ALASP | GATTCTCAAGGATTTATTTGG 2324 | GATTCTCAAGGATTTATTTGG 2324 Db 1717 alAsp | GATTCTCAAGGATTTATTTGG 2324
 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp 213 c) Db 1693 TTGACCTGTATTTCTTTGCCTAT 2264 alGluHisThrPheGluGluIle 233 Db 1633 | GATTCTCAAGGATTTATTTG 2324 | Oy 526 I | Qy 526

 | 213 | 213 Db 1693 2264 Qy 539 233 Db 1633 | 2264 Db 1693
2264 Qy 539
233 Db 1633 | 2264 Db 1693
233 Qy 539
 | 2264 DD 1633
233 QY 539 | 2264 Qy 539
233 ph 1633 | 2264 Qy 539
233 Ph 1623 | 233 Qy 539

 | 233 Qy 539 | 233 Qy 539
 | NTTATAGAGGAGCAATCAGAGATTTTTACCAT | NTTATAGAGGAGCAATCAGAGATTTTTACCAT
 | NTTATAGAGGAGCAATCAGAGATTTTTACCAT | NTTAT:AGAGGAGCAATCAGAGATTTTTACCAT | NTTATAGAGGAGCAATCAGAGATTTTTACCAT | NTTATAGAGGAGCAATCAGAGATTTTTACCAT | NTTATAGAGGAGCAATCAGAGATTTTTACCAT
 | NTTATAGAGGAGCAATCAGAGATTTTTACCAT | NTTATAGAGGAGCAATCAGAGATTTTTACCAT | NTTATAGAGGAGCAATCAGAGATTTTTACCAT | NTTATAGAGGAGCAATCAGAGATTTTTACCAT
 | NTTATAGAGGAGCAATCAGAGATTTTTACCAT | NTTATAGAGGAGCAATCAGAGATTTTTACCAT | NTTATAGAGGAGCAATCAGAGATTTTACCAT | ATTATAGAGGAGCAATCAGAATTTTTACCAT
 |
| TTGGTGAATCTATTGAAACGTTA 2435 QY 486TYTGLUGLUTY 183 QQ 486TYTGLUGLUTY 183 QQ 486 | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 Qy 506 YCGLUASPTYTGLYASPTYTTP 203 :: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTp 203 :: | GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | ### DB 1735 ####################################
 | GAGCAATCTCGTTAGAAGATGGA 2378 Db 1/35 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 YrGluAspTyrGlyAspTyrTrp 203 Db 1717 GATTCTCAAGGATTTATTTGG 2324 Db 1717 alAsp | GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :: | -::: Db 1717GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp213 :: Cy 526 Db 1693 TTGACCTGTATTTCTTTGCCTAT 2264 Qy 539 alGluHisThrPheGluGluIle 233 Db 1633 Db 1633 | GATTCTCAAGGATTTATTTGG 2324 | GATTCTCAAGGATTTATTTGG 2324
 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp 213 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp 213 | Qy 526 =: -:: -:: -:: -:: -:: -:: -:: -:: -:: -:: -:: -:: -:: -:: -:: -:: -:: | Qy 526

 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 Dy 539 Db 1633 | | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 Db 1633
 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | ATTICITIFICCIAT 2284 ATTPheGluGluIle 233 Db 1633 | hrPheGluGluIle 233 Db 1633

 | hrPheGluGluIle 233 Qy 539 | hrPheGluGluIle 233 Qy 539
 | 223 Qy 557 224 Qy 557 225 Qy 557 226 11 11 227 11 11 228 1582 229 1582 2207 207 2207 207 2207 207 2207 2207 2207 2207 2208 2207 2209 577 1220 11 2220 2207 2220 2207 2220 2207 2220 2207 2220 2207 2220 2207 2220 2207 2220 2207 2220 2207 2220 223 2220 223 2220 223 2220 223 2220 223 2220 223 2220 223 2220 223 2221 223 2222 <td>Qy 557 puTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 colored for the colo</td> <td>Qy 557 uTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Local 1582 Local 1682 Local 1683 Local 1683</td> <td>Qy 557 uTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 </td> <td>Qy 557 puTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 puTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 puTyrGluHisLeuHisAlaTyrValArgAcAccc 2207 puTyrGluHisLeuHisAlaTyrPaccal 11 puTyrGluHisLeuHisAlaTyrPaccal 273 putyrGluHisLeuHisAlaTyrPaccal 274 putyrGluHisLeuHisAlaGluHis 273 putyrGluHisLeuHisAlaGluHis 273 putyrGluHisLeuHisAlaGluHis 273 putyrGluHisLeuHisAlaGluHis 273 putyrGluHisLeuHisAlaGluHis 274 putyrGluHisleuHisLeuHisLeuHislaGluHisleuHislaGluHisle</td> <td>Qy 557 uTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 </td> <td>Qy 557 uTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Local 1582 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Lilli 11111 Lilli 11111 Lilli 11111 Lilli 1111 Lil</td> <td>Qy 557 uTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 </td> <td> Oy 577 </td> <td>223 Qy 557 224 Qy 557 225 226 227 226 227 227 227 Db 1582 1582 1582 1582 1682 168 216 1683 168 216 1684 168 216 1785 168 216 1884 216 216 1885 216 216 1885 216 216 1886 216 216 1887 216 216 1887 216 216 1888 216 216 1889 216 216 289 293 293 2907 297 297 291 293 294 292 293 294 293 294 293 294 293 294 295 297 297 297 297 297 298 297<td> Qy 557 </td><td> Qy 557 </td><td>223 Qy 557 224 Qy 557 225 Qy 557 226 1582 227 Db 1582 228 Db 1582 229 Db 1582 2207 Db 1534 2207 Db 1534 2207 Db 1534 2207 Db 1534 2207 Db 1525 2207 Db 1525 2208 Db 1492 2309 Db 1492 2312 Db 1492 232 Db 1432</td><td> Oy 557 </td><td>Qy leSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlAgarg 273 </td></td> | Qy 557 puTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 colored for the colo | Qy 557 uTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Local 1582 Local 1682 Local 1683 | Qy 557 uTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 | Qy 557 puTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 puTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 puTyrGluHisLeuHisAlaTyrValArgAcAccc 2207 puTyrGluHisLeuHisAlaTyrPaccal 11 puTyrGluHisLeuHisAlaTyrPaccal 273 putyrGluHisLeuHisAlaTyrPaccal 274 putyrGluHisLeuHisAlaGluHis 273 putyrGluHisLeuHisAlaGluHis 273 putyrGluHisLeuHisAlaGluHis 273 putyrGluHisLeuHisAlaGluHis 273 putyrGluHisLeuHisAlaGluHis 274 putyrGluHisleuHisLeuHisLeuHislaGluHisleuHislaGluHisle
 | Qy 557 uTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 | Qy 557 uTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Local 1582 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Lilli 11111 Lilli 11111 Lilli 11111 Lilli 1111 Lil | Qy 557 uTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 | Oy 577 | 223 Qy 557 224 Qy 557 225 226 227 226 227 227 227 Db 1582 1582 1582 1582 1682 168 216 1683 168 216 1684 168 216 1785 168 216 1884 216 216 1885 216 216 1885 216 216 1886 216 216 1887 216 216 1887 216 216 1888 216 216 1889 216 216 289 293 293 2907 297 297 291 293 294 292 293 294 293 294 293 294 293 294 295 297 297 297 297 297 298 297 <td> Qy 557 </td> <td> Qy 557 </td> <td>223 Qy 557 224 Qy 557 225 Qy 557 226 1582 227 Db 1582 228 Db 1582 229 Db 1582 2207 Db 1534 2207 Db 1534 2207 Db 1534 2207 Db 1534 2207 Db 1525 2207 Db 1525 2208 Db 1492 2309 Db 1492 2312 Db 1492 232 Db 1432</td> <td> Oy 557 </td> <td>Qy leSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlAgarg 273 </td> | Qy 557
 | Qy 557 | 223 Qy 557 224 Qy 557 225 Qy 557 226 1582 227 Db 1582 228 Db 1582 229 Db 1582 2207 Db 1534 2207 Db 1534 2207 Db 1534 2207 Db 1534 2207 Db 1525 2207 Db 1525 2208 Db 1492 2309 Db 1492 2312 Db 1492 232 Db 1432 | Oy 557
 | Qy leSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlAgarg 273 |
| TTGGTGAATCTAATGAAACGTTA 2435 TTGGTGAATCTATGAAACGTTA 2435 Qy 486TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: GATTCTCAAGGATTTATTTGG 2324 213GATTCTCAAGGATTTATTTGG 2324 21Asp | TTGGTGAARCTATTGAAACGTTA 2435 QY 486TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAAGATGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 yrGluAspTyrGlyAspTyrTrp 203 | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | Qy 486

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 Y:CluAspTyrGlyAspTyrTrp 203 Y:CluAspTyrGlyAspTyrTrp 203 Y:CluAspTyrGlyAspTyrTrp 203 Y:CluAspTyrGlyAspTyrTrp 203 Alasp | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YCGLUASPTYTGLYASPTYTTP 203 ::: | ### DESCRIPTION OF THE PROPERTY OF THE PROPERT | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 ":"
 | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGHASPTYIGHYASPTYITIP 203 ::: | -::: Db 1717GATTCTCAAGGATTTATTTGG 2324 | | | GATTCTCAAGGATTTATTTGG 2324 alAsp213 :: :: TGACCTGTATTTCTTTGCCTAT 2264 alGluHisThrPheGluGluIle 233 alGluHisThrPheGluGluIle 233 Db 1633
 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp 213 Db 1693 TTGACCTGTATTTCTTTGCCTAT 2264 Qy 539 alGluHisThrPheGluGluIle 233 Qy 539 alGluHisThrPheGluGluIle 233 Db 1633 | Oy 526 Oy 539 O | Qy 526 | ATTTCTTTGCCTAT 2264 |
 | ATTTCTTTGCCTAT 2264 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 AVERAGE OF THE PROPERTY OF THE | ATTTCTTTGCCTAT 2284 hrPheGluGluIle 233 Db 1633
 | hrPheGluGluIle 233 Db 1633

 | hrPheGluGluIle 233 Db 1633 | hrPheGluGluIle 233 Db 1633 | auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 1582 <td>Qy 557 leSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 leSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 l l reserProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 reserProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 reserProlleGlyCysLeuProAlaHisCTTTAGGCAATTTGGTGAGTAGA 2168 Db 1534 reserProlleGlyGlnLysProAsnIleAspVal 293 reserProlleGlyGlnLysProAsnIleAspVal 293 reserProlleGlyGlnArgAfaGlnArgTlePheLysGluAlaGluLys 313 Db 1525 reserProlleGlyGlnArgAfaGlnArgTlePheLysGluAlaGluLys 313 Db 1492</td> <td>auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 </td> <td>auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 </td> <td>20TyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 11</td> <td>auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 </td> <td>auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 </td> <td>auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 </td> <td>auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 Db 1582 Db 1582 </td> <td>auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 </td> <td>auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 lll ::: </td> <td>Qy 557 LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Lilili ::: </td> <td>auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 </td> <td>auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 ll ::: <</td> <td>Qy 10 11 <</td>
 | Qy 557 leSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 leSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 l l reserProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 reserProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 reserProlleGlyCysLeuProAlaHisCTTTAGGCAATTTGGTGAGTAGA 2168 Db 1534 reserProlleGlyGlnLysProAsnIleAspVal 293 reserProlleGlyGlnLysProAsnIleAspVal 293 reserProlleGlyGlnArgAfaGlnArgTlePheLysGluAlaGluLys 313 Db 1525 reserProlleGlyGlnArgAfaGlnArgTlePheLysGluAlaGluLys 313 Db 1492 | auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 | auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 | 20TyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 11
 | auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 | auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 | auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 | auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 Db 1582 Db 1582 | auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557
 | auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 lll ::: | Qy 557 LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Lilili ::: | auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557
 | auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 ll ::: < | Qy 10 11 < |
| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTATTGAAACGTTA 2435 | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 GY 486 1735 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | Qy 486 | Qy 486

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Db 1735 yrGluAspTyrGlyAspTyrTrp 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Property of the pr | GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YTG1UASPTYTG1YASPTYTTP 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 QY 506 QY 506 1717 GATTCTCAAGGATTTAGTTGG 2324 2324 24 526 25 26 27 27 26 27 27 26 27 27 3 26 27 27 3 26 27 27 3 26 27 28 3 26 27 29 5 39 20 5 39 20 5 39 21 30 20 20 20 20 20 20 20 20 20 20 20 20 20
 | GAGCAATCTCGTTAGAAGATGGA 2378 YGGUAASPTYTTYP 203 ::: -GATTCTCAAGGATTTATTTGG 2324 -ALASP | GATTCTCAAGGATTTATTTGG 2324 | | GATTCTCAAGGATTTATTTGG 2324 | GATTCTCAAGGATTTATTTGG 2324 alasp213 :: :: TTGACCTGTATTTCTTTGCCTAT 2264 algluHisThrPheGluGluIle 233 TTTACCAT2225 Db 1633
 | GATTCTCAAGGATTTATTTGG 2324 | Oy 526 STEP Oy 526 Oy 526 Oy 528 Oy 5 | Qy 526
 | |
 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Qy 539 2225 Db 1633 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Qy 539 2225 Db 1633 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 2225 Db 1633 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 2225 Db 1633
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 | 20TyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 | Qy 557 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1582 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Qy 577 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Qy 577 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1534 LeserProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrgGlagagagagagagagagagagagagagagagagagaga | Qy 557 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 207 27 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1582 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Qy 577 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1534 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 2168 Db 1534 LeserProIleGlyCysLeuProAlaHisCysProAsnIleAspVal 293 Db 1534 LaserProIleUThrValProPheGlyGlnLysProAsnIleAspVal 293 Cy 597 LaserProIleUThrValProPheGlyGlnLysProAsnIleAspVal 2132 Db 1525 LaserProIleUThrValProPheGlyGlnArgTlePheLysGluAlaGluLys 313 Db 1525 LametValAspGlnAlaTrpAspAlaGlnArgTlePheLysGluAlaGlaAAA 2108 Db 1492 MTT
 | 20TYTGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 | 20TYTGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 | Qy 557 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1582 Lill 11 | Qy 557 leSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1582 leSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Qy 577 leSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Qy 577 leSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1534 | 20TYrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 1
 | Qy 557 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1582 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Qy 577 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Qy 577 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1534 LeserProIleGlyCysLeuProAlaHisCrTTAGGCAATTGGTGGAGTAGA 2168 Qy 597 NxAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 Db 1534 Lill::: 11:: :: | Qy 557 LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 293 Db 1582 Lilili 111111 11111< | 20TYTGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 1 1 1 1 1 1 1 1 1 1
 | Qy 557 leSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1582 lili 111 | 20TYTGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Qy 557 10 11 <td< td=""><td>Qy LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db LeserProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 2168 Qy LeserProlleGlyCysLeuProAspAlaGlnArgIlePheLysGluAlaGluLys 2132 Qy LaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db LaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db LaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db Lilli::::::::::::::::::::::::::::::::::</td></td<> | Qy LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db LeserProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 2168 Qy LeserProlleGlyCysLeuProAspAlaGlnArgIlePheLysGluAlaGluLys 2132 Qy LaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db LaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db LaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db Lilli:::::::::::::::::::::::::::::::::: |
| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTATTGAAACGTTA 2435 Qy 486TyrGluGluTyr 183 ::: ::: GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTxp 203 | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 486 1735 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | Qy 486 | Qy 486

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 PyrGluAspTyrGlyAspTyrTrp 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 PYGLUASpTyrGlyAspTyrTrp 203 SHORT CAAGGATTAATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 Y::: | GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: -GATTCTCAAGGATTTATTTGG 2324 alAsp213 :: -TTGACCTGTATTTCTTTGCCTAT 2264 allHisThrPheGluGluIle 233 | GATTCTCAAGGATTTATTTGG 2324 | | GATTCTCAAGGATTTATTTGG 2324GATTCTCAAGGATTTATTTGG 2324
 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp213 Qy 526 :: TTGACCTGTATTTCTTTGCCTAT 2264 alGluHisThrPheGluGluIle 233 | GATTCTCAAGGATTTATTTG 2324 alAsp213 :: | Qy 526 1.1sp 213 1.1l Db 1693 TTGACCTGTATTTTTTTTTTTTTCCCTAT 2264 Qy 539 1 1 Qy 539 1 1 Db 1633 TTTTACCAT 2225 Db 1633 | Qy 526

 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 | | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Qy 539 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Qy 539 2225 Db 1633
 | ATTTCTTTGCCTAT 2264 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Qb 1633 | ATTTCTTTGCCTAT 2284 Qy 539 hrPheGluGluIle 233 Db 1633 | hrPheGluGluIle 233

 | hrPheGluGluIle 233 Qy 539 | hrPheGluGluIle 233 Qy 539
 | ### Part | 1 1 1 1 1 1 1 1 1 1
 | AUTYTG1uHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 257 258 257 258 | ### Part | 1 1 1 1 1 1 1 1 1 1 | 1 1 1 1 1 1 1 1 1 1 | 23 24 25 25 25 25 25 25 25
 | auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 | auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 | 19 15 16 17 18 19 19 19 19 19 19 19 | 1
 | 23 24 25 25 25 25 25 25 25 | auTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 25 | 1 1 1 1 1 1 1 1 1 1 | SurfyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Cy
 |
| TTGGTGAATCTATTGAAACGTTA 2435 QY 486TyrGluGluTyr 183 GAGCAATCTCGTTAGAAAGATGGA 2378 GAGCAATCTCGTTAGAAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 :: | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183TyrGluGluTyr 183 | Qy 486 GAGCAATCTCGTTAGAAGARGGA 2378 GAGCAATCTCGTTAGAAGARGGA 2378 Qy 506 YCGLUASPTYTGLYASPTYTTP 203 :: | Qy 486 GAGCAATCTCGTTAGAAGAFGGA 2378 GAGCAATCTCGTTAGAAGAFGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :: | GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 YIGIUASPTYTGIYASPTYTTP 203 III | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YTG1UASpTYTG1YASpTYTTP 203 :: | -::: | | GATTCTCAAGGATTTATTTGG 2324
 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp | GATTCTCAAGGATTTATTTGG 2324 2324 24 | Qy 526 | Oy 526
 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 | | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Db 1633
 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Qb 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | hrPheGluGluIle 233 Db 1633

 | hrPheGluGluIle 233 | hrPheGluGluIle 233
 | PUTYTG1UHISLEUHISAlaTyrValArgAlaLysLeuMetAsnalaTyrPro 253 :::::::::::::::::::::::::::::::::::: | PUTYTG1UHISLEUHISAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Db 1582 Dc 1582 Dc 1582 Dc 1582 Dc 1584 Dc 1586 Dc 1586 | PUTYTG1UHISLEUHISAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Db 1582 Db 1582 Db 1582 Db 1582 Db 1582 Db 1584 Db 1585 Db 1586 Db 1496 Db 1496
 | ### PartyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 #### PartyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 ################################### | PuTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 182 11 183 11 184 11 185 11 186 11 187 11 188 11 188 11 189 11 189 11 180 11 181 11 184 11 185 11 186 21 187 21 188 21 189 21 180 15 181 11 182 21 183 21 184 21 185 22 186 23 187 29 188 29 189 15 189 15 189 15 189 15 189 15 189 15 189 15 189< | puTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 puTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 put 1582 1182 put 1582 1182 put 1582 1182 put 1583 1582 put 1584 1582 put 1584 1582 put 1584 1582 put 1585 168 put 1584 168 put 1584 168 put 1585 168 put 1586 168 put 1587 168 put 1587 168 put 1588 168 put 1589 168 put 1588 168 put 1588 168 put 1589 168 put 1588 168 | PUTYTG1UHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Db 1582 1582 1582 Db 1584 Db 1586 Db 1496 Db 1 | ### PartyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 ### PartyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 ### PartyrGluHisLeuHisAlaTyrPro 253 ### PartyrGluHisLeuHisChalaTyrPro 253 ### PartyrGluHisLeuHisChalaTyrPro 253 ### PartyrGluHisLeuHisChalaTyrPro 253 ### PartyrGluHisLeuHisChalaTyrPro 253 ### PartyrGluHisChalaTyrPro 253 ### PartyrGluHisChal | puTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 puTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 pub 1582 put 1682 put 1682 put 1582 put 1593 put 1593 put 1593 put 1593 put 1593 put 1593 put | PUTYTG1UHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 Db 1582 Db 1582 Db 1582 Db 1582 Db 1582 Db 1584 Db 1585 Db 1584 Db 1586 Db 1486 Db 1486 | puTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 puTyrGluHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 put 1582 1182 put 1582 1182 put 1582 1182 put 1583 1182 put 1584 1182 put 1683 273 put 1684 273 put 1685 273 put 1685 273 put 1685 273 put 1686 293 put 1687 293 put 1687 293 put 1687 293 put 1688 294 put 1688 293 put 1688 293 put 1689 293 <t< td=""><td>PUTYTG1UHISLEUHISAlaTyrValArgAlaLysLeuMetAsnalaTyrPro 253 Db 1582 Db 1582 Db 1582 Db 1582 Db 1584 Db 1585 Db 1584 Db 1584 Db 1584 Db 1584 Db 1584 Db 1584 Db 1585 Db 1586 Db 1686 Db 1686</td><td>PUTYTG1UHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 </td><td>PUTYTG1UHisLeuHisAlaTyrValArgAlaLysLeuMetAsnalaTyrPro 253 Db 1582 1582 1582 1582 1582 1583 1582 1583 1583 1583 1584 1584 1585 1584 1585 1585 1586 1586 1587 1587 1587 1588
1588 1588</td><td>PUTYTGLUHISALATYTVALATGALALYSLEUMETASNALATYTPTO 253 </td></t<> | PUTYTG1UHISLEUHISAlaTyrValArgAlaLysLeuMetAsnalaTyrPro 253 Db 1582 Db 1582 Db 1582 Db 1582 Db 1584 Db 1585 Db 1584 Db 1584 Db 1584 Db 1584 Db 1584 Db 1584 Db 1585 Db 1586 Db 1686 | PUTYTG1UHisLeuHisAlaTyrValArgAlaLysLeuMetAsnAlaTyrPro 253 | PUTYTG1UHisLeuHisAlaTyrValArgAlaLysLeuMetAsnalaTyrPro 253 Db 1582 1582 1582 1582 1582 1583 1582 1583 1583 1583 1584 1584 1585 1584 1585 1585 1586 1586 1587 1587 1587 1588 | PUTYTGLUHISALATYTVALATGALALYSLEUMETASNALATYTPTO 253 |
| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTATTGAAACGTTA 2435 QY 486TyrGluGluTyr 183 QY 486TyrGluGluTyr 183 Db 1735 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 ::: ::: | Qy 486 | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 QY 526 ALASP | GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 YCGLUASPTYTGLYASPTYTTP 203 | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YTGLUASPTYTTP 203 :: | -::: -:GATTCTCAAGGATTTATTTGG 2324 -:GATTCTCAAGGATTTATTTGG 2324 29 526 21Asp | GATTCTCAAGGATTTATTTGG 2324 | GATTCTCAAGGATTTATTTGG 2324
 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alasp | GATTCTCAAGGATTTATTTGG 2324 | Qy 526 alAsp | Oy 526
 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 | | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Qy 539 Db 1633
 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 ATTTCTTTGCCTAT 2264 Qy 539 Db 1633 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | hrPheGluGluIle 233 Db 1633

 | hrPheGluGluIle 233 | hrPheGluGluIle 233 Qy 539 2225 Db 1633
 | 1 1 1 1 1 1 1 1 1 1 | LESERPROILEGLYCYSLEULEUGLYSLEUWECKASHALATYRPRO 253 LESERPROILEGLYCYSLEUPROALAHISLEULEUGLYASPMETTRGACACCC 2207 Qy 577 LESERPROILEGLYCYSLEUPROALAHISLEULEUGLYASPMETTRGAYARG 273 LIIII ::
 | | ###################################### | 1 1 1 1 1 1 1 1 1 1 | |
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 | | Db 1582 Db 1682 Db 1 | 1 1 1 1 1 1 1 1 1 1 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 L |
| TTGGTGAARCTATTGAAACGTTA 2435 TTGGTGAARCTATTGAAACGTTA 2435 | TTGGTGAARCTATTGAAACGTTA 2435 TTGGTGAARCTATTGAAACGTTA 2435 Qy 486TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAAGATGA 2378 yrGluAspTyrGlyAspTyrTrp 203 yrClaftyAspTyrTrp 203 yrClaftyAspTyrTrp 203 yrClaftyAspTyrTrp 2324GATTCTCAAGGATTTATTTGG 2324 alAsp | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 YTGLUASpTYTGLUSDTYTTP 203 :: | Qy 486 Qy 506 Q

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 yrGluAspTyrGlyAspTyrTrp 203 y:: -GATTCTCAAGGATTTATTTGG 2324 alAsp | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 YCGLUASpTyrGlyAspTyTTp 203 :: | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGLUASPTYTGLYASPTYTTP 203 :: | | GAGCAATCTCGTTAGAAGARGGA 2378 GAGCAATCTCGTTAGAAGARGGA 2378 Qy 506 ":"
 | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGLUASPTYIGLYASPTYITIP 203 ::: | | | GATTCTCAAGGATTTATTTGG 2324 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alasp
 | GATTCTCAAGGATTTATTTGG 2324 | Oy 526 Oy 529 Oy 529 Oy 529 Oy 529 Oy 527 O | Oy 526
 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Db 1633 |
 | ATTTCTTTGCCTAT 2264 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 2225 Qy 557 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633
 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | hrPheGluGluIle 233

 | hrPheGluGluIle 233 | hrPheGluGluIle 233 | LESERPFOILEGLYCYSLEUPROALAHISLEULEUGLYASPMETTRACTGGTTCAACACCC 2207 LILILI ::
 | LESERPTOILEGLYCYSLEUProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 LILILI III III III III III III III III | LESErProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 LeserProlleGlyCysLeuProAlaHisleuLeuGlyArg 273 LeserProlleGlyCysLeuProlleGlyArg 273 LeserProlleGlyCy | LESErProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | Db 1582 Db 1492 Db Db 1492 Db 1492 Db 1492 Db 1492 Db 1492 Db Db 1492 Db 1 | Db 1582 Db 1682 Db | Db 1582
 | Db 1582 Db Db 1582 Db 1682 | Db 1582 1582 1582 16 | Db 1582 Db 1682 Db Db Db Db Db Db Db D | Db 1582 Db 1682 Db | Db 1582 1582 1582 16 | Db 1582 IESErProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
 | Db 1582 1582 1582 16 | LESErProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 |
| TTGGTGAAHCTATTGAAACGTTA 2435 TTGGTGAAHCTATTGAAACGTTA 2435 Qy 486TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 GY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 PICHASPTYGLQAYASPTYTTP 203 SECOND CONTROL OF CONT | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 YGGLUASpTYrGlyAspTYrTrp 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :: | | GAGCAATCTCGTTAGAAGARGGA 2378 GAGCAATCTCGTTAGAAGARGGA 2378 Qy 506 Qy 506 Qy 506 Qy 506 1717 GATTCTCAAGGATTTAGTTGG 2324 Alsp
 | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YTG1UASpTYrG1YASpTYrTTP 203 ::: | | GATTCTCAAGGATTTATTTGG 2324 | GATTCTCAAGGATTTATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp | GATTCTCAAGGATTTATTTGG 2324 21Asp213 21-
 | GATTCTCAAGGATTTATTTG 2324 | alAsp | Oy 526
 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Db 1633
 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 2225 Oy 539 Db 1633 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633
 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 hrPheGluGluIle 233 Db 1633 2225 Oy 557 | hrPheGluGluIle 233

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 | | | | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 [|
| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTGAAACGTTA 2435 Qy 486TyrGluGluTyr 183 ::: ::: GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :: GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 YTG1UASpTYrT1y 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::

 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 YIGUAASPTYrTIP 203 ::: -GATTCTCAAGGATTATATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 alAsp | GAGCAATCTCGTTAGAAGAFGGA 2378 GAGCAATCTCGTTAGAAGAFGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YCGLUASpTYYGLYASpTYTTY 203 III QY 506 I 717 GATTCTCAAGGATTTATTTGG 2324 ALASp | GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: | GATTCTCAAGGATTTATTTGG 2324 | | GATTCTCAAGGATTTATTTGG 2324GATTCTCAAGGATTTATTTGG 2324
 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp 213 :: TTGACCTGTATTTCTTTGCCTAT 2264 Db 1693 TTGACCTGTATTTCTTTGCCTAT 2264 Qy 539 alGluHisThrPheGluGluIle 233 | GATTCTCAAGGATTTATTTG 2324 alAsp213 :: Db 1693 TTGACCTGTATTTCTTTGCCTAT 2264 alGuHisThrPheGluGluIle 233 Qy 539 alGuHisThrPheGluGluIle 233 TTTACCAT2225 TTTACCAT | Qy 526 11 Db 1693 TTGACCTGTATTTCTTTGCCTAT 2264 Db 1693 AlGUHISThrPheGluGluIle 233 Qy 539 AlGUTTACCAT 2225 Db 1633 TTTACCAT 253 Qy 557 | Oy 526 Oy 527 Oy 527 Oy 527 Oy 527 Oy 539 Oy 557 Oy 526 Oy 557 O | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233
 | | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Qy 539 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233
 | ATTTCTTTGCCTAT 2264 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 | hrPheGluGluIle 233

 | hrPheGluGluIle 233 | hrPheGluGluIle 233 | Db 1582
 | Db 1582 | Db 1582
 | Db 1582 1582 1582 1582 1682 | Db 1582 | Db 1582 | Db 1582 | Db 1582 Dc 1682 Dc 1 | Db 1582 Db 1682 Db 1 | Db 1582 Db 1534 Db 1535 Db 1 | Db 1582 Dc 1682 Dc 1
 | Db 1582 | Db 1582 Dc Dc Dc Dc Dc Dc Dc D | Db 1582 | Db Comparison
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| TTGGTGAATCTATTGAAACGTTA 2435 TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 GY 486 2378 QY 486 QY 506 1735 QY 506 1717 GATTCTCAAGGATTTATTTGG 2324 ALASP | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183TyrGluGluTyr 183 | Qy 486 GAGCAATCTCGTTAGAAGARGGA 2378 GAGCAATCTCGTTAGAAGARGGA 2378 Qy 506 :: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YTGLUASPTYTGLYASPTYTTP 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGHUASPTYTGIP 203 IIIGATTCTCAAGGATTTATTTGG 2324 ALASP | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 ;; | -::: -:GATTCTCAAGGATTTATTTGG 2324 -:GATTCTCAAGGATTTATTTGG 2324 2324 24 25 25 26 27 27 28 29 29 29 29 29 29 20 20 20 20 | | GATTCTCAAGGATTTATTTGG 2324
 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp213 | GATTCTCAAGGATTTATTTGG 2324 | Qy 526 alAsp | Oy 526 Sill Oy 526 Sill Oy 526 Sill Oy 526 Oy 526 Oy 526 Oy 526 Oy 526 Oy 527 Oy 527 Oy 528 Oy 539 Oy 557 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233
 | | ATTTCTTTGCCTAT 2264 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Qy 539 2225 Db 1633 etAsnAlaTyrPro 253 Qy 557 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Qy 539
 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Qb 1633 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 2225 Qy 557 etAsnAlaTyrPro 253 | hrPheGluGluIle 233

 | hrPheGluGluIle 233 2225 etAsnAlaTyrPro 253 Qy 539 Db 1633 Qy 557 | hrPheGluGluIle 233 Qy 539 | 182
 | LESERPTOILEGLYCYSLEUPTOALAHISLEULEUGLYASPMETTTGAACACCC 2207 QY 577 | 182
 | Db 1582 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Up 1582 Up Up Up Up Up Up Up U | LESERPFOILEGLYCYSLEUPOALAHISLEULEUGLYASPMETTTGATCACACCC 2207 QY 577 LITTACTGGTTCAACACCC 2207 QY 577 LITTACTGGTTGCAACACCC 2207 QY 577 LITTACTGGTTGCCAAGATATGCTTTAGGCAATTTGGTGGAGTAGA 2168 QY 597 LITTACTGTTGCCAAGATATGCTTTAGGCAATTTGGTGGAGTAGA 2168 QY 597 LITTACTGTTGCCAAGATATGCTTTAGGCAATTTA 2132 LITTACTGTTGCTGATACGTCGGATGAATACTTTGGATTTA 2132 QY 597 LAMETVALASPGLNALATTPASPALAGLNATGILEPheLysGluAlaGluLys 313 LITTACTGTTGATACGTCGGATGAACAGAGAAA 2108 LAMETTTCCCCTTATACGTCGATGACTGGATGAAACAGAGAAA 2108 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | DE 1582 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 CeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 CeserProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 CeserProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyGagTaGa 2168 CeserProIleGlyGcagTaGagTaGa 2168 CeserProIleGlyGlnLysProAsmIleAspVal 293 CeserProIleGlyGlnLysProIle | Db 1582 LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1582 CleSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1534 CleSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1534 CleSerProlleGlyGlorLysProAsmTeGargaga 2168 Qy 597 CleSerProlleGlyGlorLysProAsmTleAspVal 293 CleSerProlleGlyGlorLysProAsmTleAspVal 293 ClesterProlleGlyGlorLysProAsmTeGargagara 2132 ClesterProlleGlyGlorLysProAsmTeTrgGartTra 2132 ClesterProlleGlyGlorLysProAsmArgagara ClesterProlleGlyGlorLysProlleGlyGlyGlorLysProlleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG | LeserProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | 182
 | LeserProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 |
 | 182 | LESERPROILEGIYCYSLEUPROALAHISLEULEUGIYASPMETTRGATCACACCC 2207 QY LESERPROILEGIYCYSLEUPROALAHISLEULEUGIYASPMETTRGATYARG 273 |
| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTATTGAAACGTTA 2435 ::: ::: GAGCAATCTCGTTAGAAGATGGA 2378 ::: GAGCAATCTCGTTAGAAGATGGA 2378 ::: | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyTrp 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 YYGLUASpTYYGJYASPTYTTP 203 :::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 ":" | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGLUASPTYIGLYASPTYITIP 203 ::: | -::: -::: -::: -:::: -:::::::::::::::: | | GATTCTCAAGGATTTATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324
 | GATTCTCAAGGATTTATTTGG 2324 alasp213 :: :: TTGACCTGTATTTCTTTGCCTAT 2264 AGGILLHISThrPheGluGluIle 233 IITTACCAT2225 Db 1633 TTTACCAT225 lalysLeuMetAsnAlaTyrPro 253 | GATTCTCAAGGATTTATTTGG 2324 | alAsp | AlAsp
 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 | | ATTTCTTTGCCTAT 2264 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233
 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 2225 etAsnAlaTyrPro 253 ATTTCTTTGCCTAT 2264 Oy 539 Db 1633 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 | hrPheGluGluIle 233 2225 etAsnAlaTyrPro 253 Qy 539 Db 1633 Qy 557

 | hrPheGluGluIle 233 Qy 539 2225 Db 1633 2225 Qy 557 | hrPheGluGluIle 233
 | 1525 1896 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 :::
 | LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Lilli :: | LESETPTOILEGLYCYSLEUPTOALAHISLEULLEUGLYASPMETTTPGLYARG 273 LESETPTOILEGLYCYSLEUPTOALAHISLEULLEUGLYASPMETTTPGLYARG 273 LITTI LI | 1534 1525 168erProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 27 | 1534 1525 168erProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 169erProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 169erProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 169erProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 169erProIleGlyArg 273 169erProIleGlyArg 273 169erProIleGlyGlnLysProAsmIleAspVal 293 169erProIleGlyGlnLysProAsmIleAspVal 293 169erProIleGlyGlnLysProAsmIleAspVal 293 169erProIleGlyGlnLysProAsmIleAspVal 293 169erProIleGlyGlnArgIlePheLysGluAlaGluLys 313 169erProIleGlyGlnArgIlePheLysGluAlaGluLys 313 169erProIleGlyGlnArgIlePheLysGluAlaGlyLys 313 169erProIleGlyGlnArgIlePheLysGluAlaGlyLys 313 169erProIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG | 1534 1534 1635 | 1525 AMETVALASPORTAGATANCE 10 10 10 10 10 10 10 1
 | Control Cont | 1.20 | 1534 1534 168erProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 27 | 1534 1534 1635
1635 | 1534 1534 1534 1535 | 154 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 |
| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTATTGAAACGTTA 2435 ::: ::: | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAAGATGA 2378 y::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyTTp 203 ::: | Qy 486

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 YGLUASpTYrGlyAspTYrTrp 203 :: | 1735 GAGCAATCTCGTTAGAAGATGGA 2378 Db 1735 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 YrGluAspTyrGlyAspTyTTp 203 Db 1717 GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrTrp 203 :: | Db 1735 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 YCCLUASpTYYGLYASpTYTTP 203 YCCLUASpTYTGLYASPTYTTP 203 YCCLUASPTYTGATTTGG 2324 Db 1717 CATTCTCAAGGATTTATTTGG 2324 Qy 526 ALASP
 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 ":" | GAGCAATCTCGTTAGAAGATGGA 2378 YGGLUASpTyrGlyAspTyrTrp 203 :::GATTCTCAAGGATTAATTTGG 2324 alAsp | -::: Db 1717GATTCTCAAGGATTTATTTGG 2324 AlAsp 213 -: TTGACCTGTATTTCTTTGCCTAT 2264 AlGulhisThrPheGluGluIle 233 TTTACCAT 2225 AllysLeuMetAsnAlaTyrPro 253 AllysLeuMetAsnAlaTyrPro 253 AllysLeuMetAsnAlaTyrPro 253 AllysLeuMetAsnAlaTyrPro 253 AllysLeuMetAsnAlaTyrPro 253 | | GATTCTCAAGGATTTATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp
 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp213 | GATTCTCAAGGATTTATTTGG 2324 | Oy 526 Oy 528 O | Qy 526 Sill | OY 526
 | | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Db 1633 2225 Qy 557 etAsnAlaTyrPro 253 Db 1593 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 2225 Qy 557 etAsnAlaTyrPro 253 Db 1593
 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 2225 Qy 557 etAsnAlaTyrPro 253 Db 1592 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 2225 etAsnAlaTyrPro 253 ph 1502 | hrPheGluGluIle 233

 | hrPheGluGluIle 233 | hrPheGluGluIle 233 | 1534 1534 1636
1636 | Comparison | CAPACTACT 1 1 1 1 1 1 1 1 1
 | Compared to the compared to | 1 | Cy 1525 | Compared to the control of the con | Corvered Content Con | Compared to the control of the con | ESErProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | SerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273
 | Compared to the control of the con | Carper C | 1534 1534 1535 1534 1535 | LESErProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 ::: ::: |
| TTGGTGAARCTATTGAAACGTTA 2435 TTGGTGAARCTATTGAAACGTTA 2435 | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 486 yrGluAspTyrGlyAspTyrTrp 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YGLUASPTYTGLYASPTYTTP 203 ::: | Qy 486

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 PGIUASPTYrGlyAspTYrTrp 203 :::GATTCTCAAGGATTAATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 Cy 526 alAsp | GAGCAATCTCGTTAGAAGAIGGA 2378 GAGCAATCTCGTTAGAAGAIGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGAITGA 2378 GAGCAATCTCGTTAGAAGAITGA 2378 QY 506 | GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: -GATTCTCAAGGATTATTTGG 2324 -CATTCTCAAGGATTTATTTGG 2324 -CATTCTCAAGGATTTATTTGG 2324 -CATTCTCAAGGATTTATTTGG 2324 -CATTCTCAAGGATTTATTTGG 2324 -CATTCTCAAGGATTTATTTGG 2324 -CATTCTCAAGGATTTATTTGG 233 | GATTCTCAAGGATTTATTTGG 2324 | | GATTCTCAAGGATTTATTTGG 2324GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp
 | GATTCTCAAGGATTTATTTGG 2324 alAsp213 :: clinical control co | GATTCTCAAGGATTTATTTG 2324 | Qy 526 STATE | Oy 526
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 | | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Db 1633 2225 Qy 559 etAsnAlaTyrPro 253 Qy 557 | ATTTCTTTGCCTAT 2264
 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 OY 539 hrPheGluGluIle 233 Db 1633 | ###################################### | hrPheGluGluIle 233

 | hrPheGluGluIle 233 | hrPheGluGluIle 233 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273
 | LIGHT LOGIT CAMERIC 2207 Qy 577 | LESETPTOILEGLYCYSLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 PESETPTOILEGLYCYSLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 PESETPTOILEGLYCYSLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1534 Db 1534 Db 1534 Db 1534 Db 1535 Db 1536 Db 1492
 | LESETPTOILEGLYCYSLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 ::: ::: | LIGHT LOAD AND COLOR OF THE ADMINISTRATION COLOR OF THE AD | LESETPTOILEGLYCYSLEUPTOALAHISLEULEUGLYASPMETTPGLYATG 273 | LESETPTOILEGLYCYSLEUPTOALAHISLEULEUGLYASPMETTPGLYARG 273 LESETPTOILEGLYCYSLEUPTOALAHISLEULEUGLYASPMETTPGLYARG 273 Db 1534 LITHILITIES | 1 1 1 1 1 1 1 1 1 1 | LIGHT LONG LIGHT CAMERICAL 2207 1 1 1 1 1 1 1 1 1
 | LIGHT LIGH | LIGHT LONG LICHT CAPACHE 1 1 1 1 1 1 1 1 1 | LIGHT 1 1 1 1 1 1 1 1 1 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273
 | SeerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | LESETPTOILEGLYCYSLEUPTOALAHISLEULEUGLYASPMETTPGLYARG 273 |
| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTATTGAAACGTTA 2435 QY 486TyrGluGluTyr 183 QY 486TyrGluGluTyr 183 Db 1735 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YTGLUASpTYrTLP 203 :: | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 486 yrGluAspTyrGlyAspTyrTrp 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 YICHUASPTYICLY 203 III | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YICHASPTYIGLYASPTYTTP 203 :::TCTGAAGGATTAGTTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 ALASP | GAGCAATCTCGTTAGAAGAIGGA 2378 GAGCAATCTCGTTAGAAGAIGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YCGLUASpTYYGLYASpTYTTP 203 | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YYGLUASPTYTTYP 203 ::: | GATTCTCAAGGATTTATTTGG 2324 alAsp | 1 | GATTCTCAAGGATTTATTTGG 2324GATTCTCAAGGATTTATTTGG 2324
 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp 213 | GATTCTCAAGGATTTATTTG 2324 alAsp213 :: | Qy 526
 | AlAsp
 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPHeGluGluIle 233 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 | ATTTCTTTGCCTAT 2264 | ATTTCTTTGCCTAT 2264
 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 OY 539 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 | hrPheGluGluIle 233

 | hrPheGluGluIle 233 | hrPheGluGluIle 233
 | Qy 577 LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1534 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273
 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 ::: | Qy 577 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 |
 | Qy 577 | Qy 577 | | Qy 577
 | | | Cy 577 | Qy LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273
 |
| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTATTGAAACGTTA 2435 QY 486TyrGluGluTyr 183 QY 486TyrGluGluTyr 183 Db 1735 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | TTGGTGAAFCTATTGAAACGTTA 2435 TyrGluGluTyr 183 ::: ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGAA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 QY 506 QY 506 QY 506 QY 506 1717 GATTCTCAAGGATTTAGTTGG 2324 ALASP | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAAAATGC 2378 GAGCAATCTCGTTAGAAAAATGA 2378 QY 506 YCGLUASPTYTGLYASPTYTTP 203 III | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGHASPTYIGHYASPTYITIP 203 ::: | -::: -::: -:::: -::::::::::::::::::::: | 1 |
 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp213 | GATTCTCAAGGATTTATTTGG 2324 alAsp213 alAsp213 TTGACCTGTATTTCTTTGCCTAT 2264 TTGACCTGTATTTCTTTGCCTAT 2264 AGY 539 alGluHisThrPheGluGluIle 233 TTTACCAT | Qy 526 alAsp | Oy 526

 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPHeGluGluIle 233 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPROXIMATION 233 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTGCATAGCC 2267 ATTTCTGCATAGCC 2267 ATTTCTGC | ATTTCTTTGCCTAT 2264 APPHeGluGluIle 233 2225 etAsnalaTyrPro 253 etAsnalaTyrPro 253 ctasnalaTyrPro 253 pb 1582 | ATTTCTTTGCCTAT 2264
 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 | hrPheGluGluIle 233 hrPheGluGluIle 233 Db 1633 2225 etAsnAlaTyrPro 253 etAsnAlaTyrPro 253 Db 1582

 | hrPheGluGluIle 233 2225 etAsnAlaTyrPro 253 criticaturo 2507 Db 1582 | hrPheGluGluIle 233 Qy 539 | Property of the control of the contr
 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Qy 577 | Page ProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Page P | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273
 | 1 1 1 1 1 1 1 1 1 1 | Page ProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Qy 577 ProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1534 Db 1534 Db 1534 Db 1534 Db 1534 Db 1534 Db 1535 Db 1535 Db 1535 Db 1535 Db 1535 Db 1535 Db 1525 Db 1635 | ServalGlytangarangerangerangerangerangerangeranger | 1534 1534 1635 | Page ProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | SerprolleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273
 | Page ProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | Page ProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | Page ProlieGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273
273 | Qy LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Qy L |
| TTGGTGAATCTATTGAAGGTTA 2435 TTGGTGAATCTATTGAAGGTTA 2435 ::: ::: | TTGGTGAARCTATTGAAACGTTA 2435 TTGGTGAARCTATTGAAACGTTA 2435 Qy 486TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAAGATGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyTTp 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 PYGLUASpTYrGLYASpTYrTrp 203 YICLIAGAGATTAGTTTGG 2324 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyTTp 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | | |
 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 ":" | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGLUASPTYIGLYASPTYITIP 203 ::: | -::: | |
 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp | GATTCTCAAGGATTTATTTG 2324 GATTCTCAAGGATTTATTTG 2324 2 | Oy 526 STATE Oy 527 Oy 528 Oy 529 | Qy 526 Si Compare Si Compare Compa | OY 526 ANTITCTTTGCCTAT 2264 ANTITCTTTGCCTAT 2264 APPROXIMATE AND 1693 APPROXIMATE AN |
 | ATTTCTTTGCCTAT 2264 ATTTCTTGCTTCAACACC 2207 ATTTCTTCAACACC 2207 ATTTCTTCAACACC 2207 ATTTCTTCAACACC 2207 ATTTCTTCAACACC 2207 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 2225 etAsnalaTyrPro 253 Qy 557 etAsnalaTyrPro 253 Db 1582 CTGGTTCAACACCC 2207 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 PARTHER STATE STAT | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 etAsnAlaTyrPro 253 etAsnAlaTyrPro 253 etAsnAlaTyrPro 253 cTGGTTCAACACC 2207 Db 1582 | hrPheGluGluIle 233

 | hrPheGluGluIle 233 2225 etAsnAlaTyrPro 253 cTGGTTCAACACCC 2207 phrPheGluGluIle 233 Db 1633 Qy 557 Qy 557
 | hrPheGluGluIle 233 2225 etAsnAlaTyrPro 253 CTGGTTCAACACCC 2207 Dy 539 Qy 539 Qy 557 Db 1582 | SerprolleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 0y 577
 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Oy 577 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Oy 577 | Comparison of the control of the c | SerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 027 577 1 1 1 1 1 1 1 1 1 | 154 | 154
 | SerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 027 577 1 1 1 1 1 1 1 1 1 | 1525 | SerprolleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | SerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273
 | 154 | SerprolleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | SerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | Page Prolledly CysLeu Pro AlaHis Leu Leugly AspMet TrpGly Arg 273 273
 273 |
| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTATTGAAACGTTA 2435 | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAAGATGA 2378 y:GluAspTyrGlyAspTyrTrp 203 :: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyTTp 203 ::: | Qy 486

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 YCGLUASpTYTGLYASpTYTTP 203 :: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 YGLUASpTYrGlyAspTYTTP 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | Db 1735 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 III III III Qy 506 III III III Qy 506 III III III Qy 526 AlASP
 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 ":" | GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: | -::: | | GATTCTCAAGGATTTATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp
 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp | GATTCTCAAGGATTTATTTG 2324 alAsp213 TTGACCTGTATTTCTTTGCCTAT 2264 TTGACCTGTATTTCTTTGCCTAT 2264 alGluHisThrPheGluGluIle 233 TTTACCAT2225 TTTACCAT | Oy 526 | Qy 526 Sill
 | OY 526 | | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPHeGluGluIle 233 | ATTTCTTTGCCTAT 2264 Db 1693 hrPheGluGluIle 233 Db 1633 2225 Qy 557 etAsnAlaTyrPro 253 Qy 557 CTGGTTCAACACCC 2207 Db 1582
 | ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 2225 Qy 557 etAsnAlaTyrPro 253 Qy 557 ::: CTGGTTCAACACCC 2207 Db 1582 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 L633 L725 etAsnAlaTyrPro 253 E1 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 PhrPheGluGluIle 233 Db 1633 2225 etAsnalaTyrPro 253 etAsnalaTyrPro 253 CTGGTTCAACACCC 2207 Db 1582 | hrPheGluGluIle 233

 | hrPheGluGluIle 233 | hrPheGluGluIle 233
 | LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273
 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 :: | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273
 | | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | | LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273
 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 :::
 |
| TTGGTGAANCTATTGAAACGTTA 2435 TTGGTGAANCTATTGAAACGTTA 2435 Qy 486TyrGluGluTyr 183 ::: ::: ::: | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 QY 486 1735 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | Qy 486 | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 PIGLUASPTYTTP 203 STORMAGATTTATTTGG 2324 CONTROL 233 CONTRO | GAGCAATCTCGTTAGAAGAFGGA 2378 GAGCAATCTCGTTAGAAGAFGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | | GAGCAATCTCGTTAGAAGARGGA 2378 GAGCAATCTCGTTAGAAGARGGA 2378 QY 506
 | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGLUASPTYIGLYASPTYTTP 203 ::: | | | | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp 213
 | GATTCTCAAGGATTTATTTG 2324 alAsp213 :: | Qy 526 ST Qy 526 ST ST Qy 526 ST ST ST ST ST ST ST S | Oy 526 Sill Oy 539 Sill Oy 557 Sill Oy 557 Sill Oy 557 Sill Oy 557 Oy 557 Oy 557 Oy 558 | OY 526
 | | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPROXIMATE AND APPROXIMATE APPROXIMATE AND APPROXIM | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539
 | hrPheGluGluIle 233

 | hrPheGluGluIle 233 | hrPheGluGluIle 233 Qy 539 | leSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273
 | leSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | leSerProlleGlyCysLeuProAlaHiSLeuLeuGlyAspMetTrpGlyArg 273 Db 1534 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273
 | leSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1534 TGTTGCCAAGATATGCTTTAGGCAATTGGTGGAGTAGA 2168 Qy 597 TARSILEUTYTSETLEUThrValProPheGlyGlnLysProAsilleAspVal 293 | leSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | leSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1534 | LeSerProIleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1534
 | leSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | leSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 Db 1534 | leSerProlleGlyCysLeuProAlaHiSLeuLeuGlyAspMetTrpGlyArg 273
 | leSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 | LeSerProlleGlyCysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArg 273 |
| TTGGTGAATCTATTGAAACGTTA 2435 QY 486TYTGLUGLUTY 183 GAGCAATCTCGTTAGAAAGATGGA 2378 QY 486 YTGLUASPTYTTP 203 :: | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183TyrGluGluTyr 183TyrGluGluTyr 183 | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 YCGLUASPTYTGTQATTATTTGG 2324 | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGLUASPTYIGLYASPTYTTP 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 YIGLUASpTYrG1YASpTYTTP 203 | GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: | GATTCTCAAGGATTTATTTGG 2324 | |
 | GATTCTCAAGGATTTATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 Oy 526 alAsp | GATTCTCAAGGATTTATTTG 2324 alAsp213 :: | Qy 526 | Oy 526

 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPHeGluGluIle 233 | | ATTTCTTTGCCTAT 2264 ATTTCTTTTGCCTAT 2264 ATTTCTTTTGCCTAT 2264 ATTTCTTTTGCCTAT 2264 ATTTCTTTTGCCTAT 2264 ATTTCTTTTGCCTAT 2264 ATTTCTTTTGCCTAT 2264 ATTTCTTTTTGCCTAT 2264 ATTTCTTTTTGCCTAT 2264 ATTTCTTTTGCCTAT 2264 ATTTCTTTTTTTTGCCTAT 2264 ATTTCTTTTTGCCTAT 2264 ATTTCTTTTTTT | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APP 539 APP 539 APP 539 APP 539 APP 539 APP 539 APP 540 APP 557 CTGGTTCAACACCC 2207 APP 557 OV 577 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPHeGluGluIle 233
 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 hrPheGluGluIle 233 Db 1633 2225 Qy 557 etAsnAlaTyrPro 253 ETGGTTCAACACCC 2207 Ov 577 | ATTICULAR 2004 Qy 539 hrPheGluGluIle 233 Db 1633

 | hrPheGluGluIle 233 | hrPheGluGluIle 233 Qy 539 | IAMETVALASPGIDALATEPASPALGCINSPERING 2/3 Db 1534 Db 1535 Db 1535 Db 1535 Db 1536 Db 153
 | Db 1534 TrAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 This: This | Db 1534 THE TOTAL COLLEGE TO THE CO | Db 1534 THE TOTAL COLLEGE TO SHEEL THE TOTAL COLLEGE TO THE TOTAL COLLE | Db 1534 TYPE TO LEGIT TO LEGIT TO SEPRECT POLYARY THE HILL HILL HILL HILL HILL HILL HILL HI | Db 1534 Db 1535 Db 1536 Db 1492 Db 1492 Db 1492 | Db 1534 TrAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 TrasnLeuTyrSerLeuThrValProPheGlyGlnLysProAspVal 293 TrasnLeuT | Db 1534 TrAsnLeuTyrSerLeuThrValProPheGlyGlnLysProPasnIleAspVal 293 TrAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 TrasnLeuTyrSerLeuThrValProPheGlyGlnLysProAspVal 293 TrasnLeuThrValProPheGlyGlnLysProAspVal 293 TrasnLeuThrValPro | Db 154
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| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTGAAACGTTA 2435 Qy 486TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: GATTCTCAAGGATTATTTGG 2324 204 506 1717 -GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAAGATGA 2378 Qy 486 yrGluAspTyrGlyAspTyrTrp 203 yrGluAspTyrGlyAspTyrTrp 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyTrp 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 yrGluAspTyrGlyAspTyrTrp 203 yrGluAspTyrGlyAspTyrTrp 203 yrGluAspTyrGlyAspTyrTrp 203 yrGluAspTyrGlyAspTyrTrp 203 yrGluAspTyrGlyAspTyrTrp 203 Db 1717 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyTTp 203 :: | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YTG1UASPTYTG1YASPTYTTP 203 ::: |
 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 ":" | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGLUASPTYIGLYASPTYITIP 203 ::: | -::: | |
 | GATTCTCAAGGATTTATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 213 | GATTCTCAAGGATTTATTTG 2324 GATTCTCAAGGATTTATTTG 2324 213 213 214 215 217 217 217 218 219 2264 227 2264 227 227 228 238 249 259 257 261 277 287 287 287 287 287 287 28 | Oy 526 Oy 529 O | Qy 526
 | OY 526 ANTITCTTTGCCTAT 2264 ANTITCTTTGCCTAT 2264 APPROACH 223 APPROACH 223 APPROACH 223 APPROACH 223 APPROACH 223 APPROACH 225 APPROACH 225
APPROACH 2207 APPROA | | ATTTCTTTGCCTAT 2264 ATTTCTTTTGCCTAT 2264 ATTTCTTTTGCCTAT 2264 ATTTCTTTTGCCTAT 2264 ATTTCTTTTGCCTAT 2264 ATTTCTTTTGCCTAT 2264 ATTTCTTTTGCCTAT 2264 ATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 OY 539 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 PARPHEGLUGILIE 233 ADD 1633 CTGGTTCAACACCC 2207 Oy 577 Oy 577 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633
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 | hrPheGluGluIle 233 Db 1633 | hrPheGluGluIle 233 | INTERPRETABLE TO THE TOTAL TOT
 | | IHIHI :: | INTERPOLATION OF THE PROPERTY | | |
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 | | | | Db TransleuTyrSerLeuThrValPropheGlyGlnLysProAsnIleAspVal 293 Lilli:::
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| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTGAAACGTTA 2435 TyrGluGluTyr 183 ::: ::: | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAAGATGA 2378 GAGCAATCTCGTTAGAAAGATGA 2378 | Qy 486 | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 Db 1735 y::GATTCTCAAGGATTTATTTGG 2324 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 YGGLUASpTYrGlyAspTYrTrp 203 ::: | GAGCAATCTCGTTAGAAGAITGGA 2378 GAGCAATCTCGTTAGAAGAITGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :: |
 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 QY 506 QY 506 QY 506 QY 506 1717 GATTCTCAAGGATTTAGTTGG 2324 QY 526 2118 2119 213 TTGACCTGTATTTCTTTGCCTAT 2264 QY 526 214 215 217 217 218 219 219 220 221 221 231 24 24 25 26 26 27 27 27 27 27 27 27 27 | GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: | | | GATTCTCAAGGATTTATTTGG 2324GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp
 | GATTCTCAAGGATTTATTTGG 2324 2324 24 | GATTCTCAAGGATTTATTTG 2324 GATTCTCAAGGATTTATTTG 2324 2 | Qy 526 | Oy 526 Sill Oy 526 Oy 539 Oy 557 Oy | OY 526
 | | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPHeGluGluIle 233 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 2225 etAsnAlaTyrPro 253 ::: Oy 557 etBertTroGlvArg 273 Db 1582 CTGGTTCAACACCC 2207 SDMetTroGlvArg 273 Db 1582 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539
 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | hrPheGluGluIle 233

 | hrPheGluGluIle 233 | hrPheGluGluIle 233 | INTERPRETARE TO THE TOTAL TOTA
 | Db 1534 Db 1536 Db 1536 Db 1536 Db 1536 Db 1536 Db 1536 Db 1525 Db 1 | Db 1534 | INTERPRETABLE CONTRACTOR OF THE PROPERTY OF TH | 1 1 1 1 1 1 1 1 1 1 | Db 1534
 | Db 1534 | Db 154 | Db 1534 Db 1535 Db 1525 Db 1 | Db 1534 Db 1535 Db 1435 Db Db 1435 Db Db 1435 Db Db Db Db Db Db Db D | Db 154
 | Db 154 | Db 1534 Db 1535 Db 1535 Db 1525 Db 1492 Db Db 1492 Db Db Db Db Db Db Db D | Db 154 | Db |
| TTGGTGAANCTATTGAAACGTTA 2435 TTGGTGAANCTATTGAAACGTTA 2435 QY 486TyrGluGluTyr 183 GAGCAATCTCGTTAGAAAGATGGA 2378 QY 486 yrGluAspTyrGlyAspTyrTrp 203 :: Qy 506 alAsp | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 486 1735 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 YICHASPTYTTP 203 III | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGLUASPTYTGLYASPTYTTP 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGHUASPTYTGIPAGAAGATTGATTTGG 2324 ALASP | GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 :::: | GATTCTCAAGGATTTATTTGG 2324 | |
 | GATTCTCAAGGATTTATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 Qy 526 | GATTCTCAAGGATTTATTTG 2324 alAsp213 :: | Qy 526 | Oy 526

 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPHeGluGluIle 233 | | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPHeGluGluIle 233 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APP 539 hrPheGluGluIle 233 2225 etAsnAlaTyrPro 253 etAsnAlaTyrPro 253 cTGGTTCAACACCC 2207 spMetTrpGlyArg 273 Db 1582 CTGGTTCAACACCC 2207 Oy 577
 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPROXIMATE 233 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 hrPheGluGluIle 233 Db 1633 | Aniilitic Clar 220% Aniilitic Clar 220% Aniilitic Clar 233 Aniilitic Clar 233 Aniilitic Clar 2225 Aniilitic Clar </td <td>hrPheGluGluIle 233</td> <td>hrPheGluGluIle 233 Qy 539 </td> <td>TOTAL TOTAL CONTROL TO THE TOT</td> <td>INTERPOLATION IN THE PROPERTY OF THE PROPERTY</td> <td>TOTAL TOTAL TOTAL</td> <td>TTGTTGCCAAGATATGCTTTAGGCAATTGGTGGAGTAGA 2168 Qy 597 TASSILeUTyrSerLeuThrValProPheGlyGlnLysProAssIleAspVal 293 : : : : : : : : : : : : : : : </td> <td>ATTTTGTTGCCAAGATATGCTTTAGGCAATTGGTGGAGTAGA 2168 Qy 597 10 10 10 10 10 10 10 10 10 10 10 10 10 1</td> <td>ATTTTTGTTGCCAAGATATGCTTTAGGCAATTGGTGGAGTAGA 2168 29 597 10 10 10 10 10 10 10 10 10 10 10 10 10 1</td> <td>TOTAL TOTAL TOTAL</td> <td>TOTAL TOTAL CONTROL OF THE PROPERTY OF THE PRO</td> <td> 134 </td> <td> 194 </td> <td> 134 137 138 139</td> <td> 134 </td> <td> 153 153 154 155
155 155</td> <td> 133 134 135 136 137 136 137 136 137 136 137 136 136 136 136 136 136 137 136</td> <td>AVAILABET PROPERTY OF THE PROP</td> | hrPheGluGluIle 233 | hrPheGluGluIle 233 Qy 539 | TOTAL TOTAL CONTROL TO THE TOT
 | INTERPOLATION IN THE PROPERTY OF THE PROPERTY | TOTAL | TTGTTGCCAAGATATGCTTTAGGCAATTGGTGGAGTAGA 2168 Qy 597 TASSILeUTyrSerLeuThrValProPheGlyGlnLysProAssIleAspVal 293 : : : : : : : : : : : : : : : | ATTTTGTTGCCAAGATATGCTTTAGGCAATTGGTGGAGTAGA 2168 Qy 597 10 10 10 10 10 10 10 10 10 10 10 10 10 1 | ATTTTTGTTGCCAAGATATGCTTTAGGCAATTGGTGGAGTAGA 2168 29 597 10 10 10 10 10 10 10 10 10 10 10 10 10 1 | TOTAL | TOTAL TOTAL CONTROL OF THE PROPERTY OF THE PRO | 134
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| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTATTGAAACGTTA 2435 QY 486TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 QY 486 yrGluAspTyrGlyAspTyrTrp 203 ::: | TTGGTGAARCTATIGAAACGTTA 2435 TyrGluGluTyr 183 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyTrp 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 :::GATTCTCAAGGATTTAGTTGG 2324 GATTCTCAAGGATTTAGTTTGG 2324 209 526 21Asp | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 ;; -GATTCTCAAGGATTTATTTGG 2324 alAsp | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGLUASPTYIGLYASPTYITTP 203 ::: | -:::: | |
 | GATTCTCAAGGATTTATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 213 | GATTCTCAAGGATTTATTTG 2324GATTCTCAAGGATTTATTTG 2324 213 214 215 217 213 215 216 214 217 217 217 217 217 217 217 217 217 217 | Qy 526 alAsp | Oy 526

 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPLICATION OF 1693 ATTTCTTTGCCTAT 2264 OY 539 APPLICATION OF 1633 CTGGTTCAACACCC 2207 CTGGTTCAACACCC 2207 CTGGTTCAACACCC 2207 OY 577 SMMetTrpGlyArg 273 Dy 1524 | AUTTCTTTGCCTAT 2264 AUTTCTTTGCCTAT 2264 AUTTCTTTGCCTAT 2264 AUTTCTTTGCCTAT 2264 AUTTCTTTGCCTAT 2264 AUTTCTTTGCCTAT 2264 AUTTCTTTGCLUGILILE 233 AUTTCTTTGCLUGILILE 233 AUTTCTTGATCTAACACCC 2207 CTGGTTCAACACCC 2207 CTGGTTCAACACCC 2207 AUTTCTTGGTLUGILILE 273 AUTTCTTGATCTAACACCC 2207 AUTTCTTGGTTCAACACCC 2207 AUTTCTTGGTTCAACACCC 2207 AUTTCTTGGTTCAACACCC 2207 AUTTCTTGGTTCAACACCC 2207 AUTTCTTGGTTCAACACCC 2207 AUTTCTTTGGTTCAACACCC 2207 AUTTCTTTGGTTCAACACCC 2207 AUTTCTTTGGTTCAACACCC 2207 AUTTCTTTGGTTCAACACCC 2207 AUTTCTTTTGGTTCAACACCC 2207 AUTTCTTTTGGTTCAACACCC 2207 AUTTCTTTTGGTTCAACACCC 2207 AUTTCTTTTGGTTCAACACCC 2207 AUTTCTTTTGGTTCAACACCC 2207 AUTTCTTTTGGTTCAACACCC 2207 AUTTCTTTTTGGTTCAACACCC 2207 AUTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCCTAT 2264 ATTTCTTTGCCCTAT 2264 ATTTCTTGCTTCAACACCC 2207 ATTTCTTGCTTCAACACCC 2207 ATTTCTTGCTTCAACACCC 2207 ATTTCTTGCTTCAACACCC 2207 ATTTCTTGCTTCAACACCC 2207 ATTTCTTGCTTCAACACCC 2207 ATTTCTTTGCTTCAACACCC 2207 ATTTCTTTGCTTCAACACCC 2207 ATTTCTTTGCTTCAACACCC 2207 ATTTCTTTGCTTCAACACCC 2207 ATTTCTTTGCTTTGCTTCAACACCC 2207 ATTTCTTTTGCTTCAACACCC 2207 ATTTCTTTTGCTTCAACACCC 2207 ATTTCTTTTGCTTTGCTTTAACACCC 2207 ATTTCTTTTGCTTTGCTTATCAACACCC 2207 ATTTCTTTTGCTTTGCTTTAACACCC 2207 ATTTCTTTTGCTTTAACACCC 2207 ATTTCTTTTGCTTTTGCTTAACACCC 2207 ATTTCTTTTTGCTTTTGCTTTAACACCC 2207 ATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 hrPheGluGluIle 233 Db 1633 2225 etAsnAlaTyrPro 253 etAsnAlaTyrPro 253 cTGGTTCAACACCC 2207 SpMetTrpGlyArg 273 Db 1582
 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 OY 539 hrPheGluGluIle 233 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 PARTHCTTTGCCTAT 2264 QY 539 DD 1633 ATTTCTTTGCCTAT 2273 DD 1582 CTGGTTCAACACCC 2207 CTGGTTCAACACCC 2207 QY 577 SPMetTrpGlyArg 273 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | hrPheGluGluIle 233 hrPheGluGluIle 233 Db 1633

 | hrPheGluGluIle 233 | hrPheGluGluIle 233 Qy 539
 | TASSILEUTYTSETLEUThrValProPheGlyGlnLysProAssIleAspVal 293 | AVASnLeuTyrSerLeuThrValPropheGlyGlnLysProAsnIleAspVal 293
 | PAPETT COLORAGATAT COLORAGATAT GOT GARACTAGA 2168 QY 597 1 | Cy 597 | ATTTTTGTTGCCAAGATATGCTTTAGGCAATTGGTGGAGTAGA 2168 Qy 597 Qy 597 Qy 597 Qy 597 Qy 597 Qy 615 | ATTTTTGTTGCCAAGATATGCTTTAGGCAATTGGTGGAGTAGA 2168 Qy 597 Qy 615 | PATTTTTGTTGCCAAGATATGCTTTAGGCAATTGGTGGAGTAGA 2168 Qy 597 1
 | Control Cont | Cy 597 | 297 | Cy 597
 | 197 | 297 | Cy 597 | ATTTT |
| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTGAACGTTA 2435 ::: GAGCAATCTCGTTAGAAGATGGA 2378 QY 486 YCGLUASPTYTGLYASPTYTTP 203 ::: -GATTCTCAAGGATTAATTTGG 2324 | TTGGTGAAFCTATTGAAACGTTA 2435 TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAAGATGA 2378 ::: GAGCAATCTCGTTAGAAGATGA 2378 | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyTTp 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 yrGluAspTyrGlyAspTyrTrp 203 y:: -GATTCTCAAGGATTTATTTGG 2324 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 YGIUASpTYrGIYASpTYTTP 203 :::GATTCTCAAGGATTAGTTTGG 2324 alAsp | GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 ":" | GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: | -::: | |
 | GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp | GATTCTCAAGGATTTATTTG 2324 GATTCTCAAGGATTTATTTG 2324 2 | Oy 526 Oy 529 O | Oy 526
 | OY 526
 | | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPROCULT 2664 APPR | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPROACH | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 AV 539 ATTTCTTTGCCTAT 2264 AV 539 ATTTCTTTGCCTAT 2264 AV 539 ATTTCTTTGCCTAT 2264 AV 539 AV 557 AV 577 BOMCTTCGACACCC 2207 AV 577 AV | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 PhrPheGluGluIle 233 ADD 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633
 | hrPheGluGluIle 233

 | hrPheGluGluIle 233 | hrPheGluGluIle 233 | AMETVALASPOIDALATEPASPALAGIANATGETEGAGTAGA 2168 QY 597 STASSILEUTYRSERLEUTHRVALPROPHEGLYGLILLYSPROASSILLEASPVAL 293 Db 1525 AMETVALASPOIDALATEPASPALAGINARGILEPHELYSGLUALAGILLYS 313 Db 1525 QY 615
 | PROTECCAAGANATGCTTTAGGCAATTGGTGAGTAGA 2168 Qy 597 WASNLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 ::: | PTETTGCCAAGATATGCTTTAGGCAATTGGTGGAGTAGA 2168 Qy 597 TASTLEUTYTSETLEUThrValProPheGlyGlnLysProAsnIleAspVal 293 ::: ::: ::: ::: ::: ::: | AMETTT | THETTICCAAGATATIGCTTTAGGCAATTIGGTGAGTAGA 2168 QY 597 TASSILEUTYTSETLEUTHTVALPTOPHEGLYGLILLYSPTOASSILLEASPVAL 293
 | PATTT | PTETTGCCAAGATATGCTTTAGGCAATTGGTGGAGTAGA 2168 QY 597 PASSILEUTYrSerLeuThrValProPheGlyGlnLysProAssIleAspVal 293 | PATEUR CCAAGAIAIGCTTTAGGCAATTGGTGAGTAGA 2168 QY 597 IXASNLEUTYR SERLEUTHRVALP FOP HEGLYGLILLYS PROASNILEAS PVAL 293 | Qy 597 CASSILEUTYrSerLeuThrValProPheGlyGlnLysProAssIleAspVal 293 Qy 597 CASSILEUTYrSerLeuThrValProPheGlyGlnLysProAssIleAspVal 293 Db 1525 CASSILEUTYrSerLeuThrValProPheGlyGlnLysProAssIleAspVal 293 Db 1525 CASSILEUTYRSERLEUTHATACGTCGGATGAATACTTGGATTTA 2132 Db 1525 CASSILEUTYRSERLEUTHATACGTCGGATGAATACTTGGATTTA 2132 Qy 615 CASSILEUTYRSERLEUTHATACGTCGGATGAATACTTGGATTTA 2132 Qy 615 CASSILEUTYRSERLEUTHATACGTCGGATGAATACTTGGATACGAGAAA 2108 Db 1492 CASSILEUTYRSERLEUTHATACGTCGGATGAATACTTGGATGAGAAA 2108 Db 1492 CASSILEUTYRSERLEUTHATACGTCGGATGAGAAA 2108 Db 1492 CASSILEUTYRSERLEUTHATACGTCGGATGAATACTTGGATGAGAAA 2108 Db 1492 CASSILEUTYRSERLEUTHATACGTCGGATGAATACTTGGATTTA 2132 Db 1492 CASSILEUTYRSERLEUTHATACGTCGGATGAATACTTGGATGAGAAAA 2108 DB 1492 CASSILEUTYRSERLEUTHATACGTCGGATGAATACTTGGATGAGAAAA 2108 DB 1492 CASSILEUTYRSERLEUTHATACGTCGGATGAATACTTGGATGTAATACTGAGAGAATACTTGGATGTAATACTGAGAGAGA | 0y 597 1xAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 Qy 597 1xAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 Db 1525 11:::::::::::::::::::::::::::::::::::
 | THE TIGGE CAAGATATIGCTTTTAGG AATTIGGT GAGTAGA | Qy 597 | THE TICC CAAGATATICCTT AGGC AATTICGT GAGTAGA 2168
2168 2168 | 297 298 | QY ITASILeuTyrSerLeuThrValProPheGlyGlnLysProAssIleAspVal 293 ::: ::: ::: |
| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTGAAACGTTA 2435 TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAGATGGA 2378 QY 486 yrGluAspTyrGlyAspTyrTrp 203 ::: -GATTCTCAAGGATTAATTTGG 2324 | TTGGTGAARCTATGAAAACGTTA 2435 TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAAGATGA 2378 | Qy 486 | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGA 2378 QYGLUASpTYTGTAGAAGATGA 2378 YCGLUASpTYTGTAGAAGATGA 2378 YCGLUASpTYTGTAGAAGATGA 2378 QY 506 YCGLUASPTYTGTATTTGG 2324 QY 506 1717 GATTCTCAAGGATTTATTTGG 2324 QY 526 alAsp | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Profile Pr | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 yrGluAspTyrGlyAspTyrTrp 203 yrGluAspTyrGlyAspTyrTrp 203 yrGATCTCAAGGATTTATTTGG 2324 Db 1717 234 Qy 526 alAsp | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 :::
 | GAGCAATCTCGTTAGAAGATGGA 2378 QYG1UASpTyrGlyAspTyrTrp 203 ::: -GATTCTCAAGGATTAATTTGG 2324 | | | GATTCTCAAGGATTTATTTGG 2324GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp | GATTCTCAAGGATTTATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 Oy 526 1.1
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 | OY 526 |
 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPHeGluGluIle 233 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 2225 ethsnAlaTyrPro 253 ::: CTGGTTCAACACCC 2207 spMetTTpG1yArg 273 ct Oy 577 spMetTTpG1yArg 273 Db 1534 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 hrPheGluGluIle 233 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633
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 | hrPheGluGluIle 233 | hrPheGluGluIle 233 | PASSILEUTYTSerLeuThrValPropheGlyGlnLysProAssIleAspVal 293
 | TASSILEUTYTSETLEUTHTVALPFORMEGIYGINLYSPTOARSILEASPUAL 293 Db 1525 LAMETVALASPALAGINARGILEPHELYSGINARGILLYS 313 Db 1492 | WASSILeuTyrSerLeuThrValProPheGlyGlnLysProAssIleAspVal 293 Qy 597 .:: ::: ::: ::: .:: ::: Db 1525 .:: ::: 2132 .:: ::: Qy 615 .aMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Qy 615 .aMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db 1492 | PARSILEUTYTSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293
 | PARTITITION OF THE PROPERTY OF | INASNLEUTYrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 Qy 597 III.:: ::: ::: ::: ::: 2132 ::: ::: Db 1525 ::: ::: 2132 ::: ::: Qy 615 ::: ::: : : : ::: ::: : ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::: :::: :::: ::::: :::: ::::: :::: ::::: :::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::: ::::: ::::: | PASSILEUTYTSETLEUTHTVALPTOPHEGLYGINLYSPTOASSILEASPVAL 293 | PASSILEUTYTSETLEUTHTVAIPTOPHEGIYGINLYSPTOASSIILEASPVAI 293 | 123 Qy 597 124 Qy 597 125 Qy 597 125 Qy 597 125 Qy 597 125 Qy 597 126 Qy 615 127 Qy 615 3ATTT 11 11 11 11 11 11 11 11 12 Qy 627 11SerValGlyLeuProAsnMet Qy 627 | WASSILEUTYrSerLeuThrValProPheGlyGlnLysProAssIleAspVal 293 Qy 597
 | xAssnLeuTyrSerLeuThrValPropheGlyGlnLysProAssnIleAspVal 293 Qy 597 | 27 1 1 1 1 1 1 1 1 1 | 123. CONTROL LA ROCCATA TROCCATA TR | xAssnLeuTyrSerLeuThrValProPheGlyGlnLysProAssnIleAspVal 293 0y 597
 | PARSILEUTYTSETLEUTHYVALPYOFACHTAGUSTAGAATACTGAATTACCGCCCCC 2048 Qy ARSILEUTYTSETLEUTHYVALPYOFACHTAGUSTAGAATACTGAATACTTCAGCCCCC 2048 Qy LAMETVALASpGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 |
| TTGGTGAANCTAATGAAACGTTA 2435 TTGGTGAANCTAATGAAACGTTA 2435 TyrGluGluTyr 183 ::: 2378 QY 486 PYGLUASPTYTGTAGAAAGATGGA 2378 QY 506 YGLUASPTYTGTAATTGGA 2324 QY 506 PYGLUASPTYTGTATTTGG 2324 QY 506 | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | Qy 486 | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 YGGLUASpTYrTLP 203 ::: -GATTCTCAAGGATTAATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
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Oy 539 Oy 539 Oy 539 Oy 539 Oy 557 Oy 557 Oy 557 Oy 557 Oy 557 Oy 577 O | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPROXIMATE 233 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPROACH 233 | ATTTCTTTGCCTAT 2264 hrPheGluGluIle 233 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 hrPheGluGluIle 233 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633
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 | hrPheGluGluIle 233 | hrPheGluGluIle 233 Qy 539 | vAssiLeuTyrSerLeuThrValProPheGlyGlnLysProAssiTleAspVal 293 Qy 597 ::: ::: ::: ::: 1::: Db 1525 :::
 | urAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 Qy 597 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : | Qy 597 INTERPRETABLE OF THE PROPRIEGIZATION P | Qy 597 | Qy 597 It AssnLeuTyrSerLeuThrValProPheGlyGlnLysProAssnIleAspVal 293 It i::::::::::::::::::::::::::::::::::::
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| TTGGTGAATCTATTGAAACGTTA 2435 TTGGTGAATCTATTGAAACGTTA 2435 QY 486TyrGluGluTyr 183 GAGCAATCTCGTTAGAAAGATGGA 2378 QY 486 yrGluAspTyrGlyAspTyrTrp 203 ::: Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: Qy 506 1717GATTCTCAAGGATTTATTTGG 2324 QY 526 alAsp | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 | Qy 486 | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyTTp 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 YCGLUASPTYTGLYASPTYTTP 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: -GATTCTCAAGGATTTATTTGG 2324 204 526 alAsp | -::: -::: -::: -:::: -:::::: -::::::::: | ::: |
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 | hrPheGluGluIle 233 hrPheGluGluIle 233 Db 1633 2225 etAsnAlaTyrPro 253 etAsnAlaTyrPro 253 CTGGTTCAACACCC 2207 spMetTrpGlyAGTACA 2168 Db 1582 ATTGGTGCAGTACA 2168

 | hrPheGluGluIle 233 | hrPheGluGluIle 233 Qy 539 | Qy 597 xAssnLeuTyrSerLeuThrValProPheGlyGlnLysProAssnIleAspVal 293 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
 | AVASSILEUTYTSETLEUTHTValPropheGlyGlnLysProAssIleAspVal 293 QY 59/ 1 : : : : : : : : : : : : : : : : | 17 xAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 | TRASNLEUTYTSETLEUTHTVAIPTOPHEGIYGINLYSPTOASNIIEASPVAI 293 | ATTTGAAACAGAGAAAA 2108
 | YEASHLEUTYTSETLEUTHTVAIPTOPHEGIYGINLYSPTOASSIILEASPVAL 293 QY 59/ YEASHLEUTYTSETLEUTHTVAIPTOPHEGIYGINLYSPTOASSIILEASPVAL 293 Db 1525 YEASHLEUTYTATACGTCGGATGAATACTTGGATTTA 2132 Db 1525 YEASHLEUTYTATACGTCGGATGAATACTTGGATTTA 2132 QY 615 YEASHLEUTYTATACGTCGGATGAATACGAGGAATA 2108 Db 1492 YATTT | 1xAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 0y 597 1 1 1 1 1 1 1 1 1 1 | 1 Year Valley of Propending Office Server (Street Fig. 1) 0.9 | YEASHLEUTYrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 09 597 1 : : : : : : : : : : : : : : | YEASHLEUTYrSerLeuThrValProPheGlyGlnLysProAshIleAspVal 293 Qy 597 1 1 1 1 1 1 1 1 1 1
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| TTGGTGAATCTAATGAAACGTTA 2435 TTGGTGAATCTATGAAACGTTA 2435 ::: GAGCAATCTCGTTAGAAGATGGA 2378 QY 486 YGLUASPTYTGLYASPTYTTP 203 ::: -GATTCTCAAGGATTATTTGG 2324 | TTGGTGAAFCTATTGAAACGTTA 2435 TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAAGATGA 2378 QY 486 yrGluAspTyrGlyAspTyrTrp 203 ::: GATTCTCAAGGATTTATTTGG 2324 AlAsp | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyTTp 203 ::: | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 yrGluAspTyrGlyAspTyrTrp 203 yrGluAspTyrGlyAspTyrTrp 203 yrGluAspTyrGlyAspTyrTrp 203 yrGluAspTyrGlyAspTyrTrp 203 yrGluAspTyrGAGGATTATTGG 2324 Qy 506 1717 alAsp | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 YrGluAspTyrGlyAspTyTTp 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 ;; | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGLUASPTYTGLYASPTYTTP 203 ::: | -::: | |
 | GATTCTCAAGGATTTATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 213 | GATTCTCAAGGATTTATTTGG 2324GATTCTCAAGGATTTATTTGG 2324 213 213 214 2264 2264 2264 2264 227 2264 227 2286 238 248 258 258 258 258 268 268 278 278 278 278 278 278 278 278 278 27 | Oy 526 STATE | Alasp
 | OY 526 | | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTGTTGCCTAT 2264 ATTTGTTGCAACACCC 2207 ATTTGGTTGCAAGA 2168 Db 1593 ATTTGGTTGCAAGA 2168 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPROCRAT 2264 APPROCRAT 2264 APPROCRAT 2264 APPROCRAT 233 APPROCRAT 2264 APPRO | ATTTCTTTGCCTAT 2264 ATTTCTTTGCTGAGAGA 2168 ATTTCGTTGGAGTAGA 2168
 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 PARTHEGIUGILIE 233 ADD 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | hrPheGluGluIle 233 hrPheGluGluIle 233 hrPheGluGluIle 233 Db 1633

 | hrPheGluGluIle 233 | hrPheGluGluIle 233 Qy 539 | WASNLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 293 .:: :: Db 1525 .::
 | IXASnLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 | IXASNLEUTYrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293
 | xAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 293 ::: ::: :: ::: :::::::::::::::::::::::::::::::::::: | AVASNLEUTYrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 293 | IXASDLEUTYrSerLeuThrValProPheGlyGlnLysProAsDIleAspVal 293 293 : : : : : : : : : : : : : : : : : : : : : : : : : : : : | IXASNLEUTYrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 293 : : : : : : : : : : : : : : : : : : | xAssLeuTyrSerLeuThrValProPheGlyGlnLysProAssIleAspVal 293 293
 | IXASNLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : ::: : ::: : ::: : ::: : ::: : ::: : ::: : ::: : ::: : ::: : ::: : ::: : ::: : ::: : :::: : :::: : :::: : :::: : :::: : ::::::: ::::::: :::::: ::::::: :::::: :::::::: ::::::: :::::::: ::::::: ::::::::: :::::::: :::::::::: :::::::: ::::::::::: :::::::: :::::::::::: :::::::: :::::::::::::::::::::::::::::::::::: | IXASDLEUTYrSerLeuThrValProPheGlyGlnLysProAsDIleAspVal 293 293 | nrAsnLeuTyrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 29
 | | IXASNLEUTYrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 | INASNLEUTYNSETLEUTHNVALPROPHEGLYGINLYSPROASNIIEASPVAL 293 29 | IXASNLEUTYrSerLeuThrValProPheGlyGlnLysProAsnIleAspVal 293 ::: ::: ::: ::: ::: ::: |
| TTGGTGAATCTAATGAAACGTTA 2435 TTGGTGAATCTGAATGGAACGTTA 2435 | TTGGTGAARCTATGAAACGTTA 2435 TyrGluGluTyr 183 ::: GAGCAATCTCGTTAGAAAGATGA 2378 ::: | Qy 486 | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 :::

 | TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 YCGLUASPTYTGLYASPTYTTP 203 :: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 PIGLUASPTYTTP 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGARGGA 2378 GAGCAATCTCGTTAGAAGARGGA 2378 QY 506 | GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YIGLUASPTYTGLYASPTYTTP 203 ::: -GATTCTCAAGGATTTATTTGG 2324 | | | GATTCTCAAGGATTTATTTGG 2324GATTCTCAAGGATTTATTTGG 2324
 | GATTCTCAAĞĞATTTATTTĞĞ 2324 GATTCTCAAĞĞATTTATTTĞĞ 2324 213 | GATTCTCAAGGATTTATTTG 2324GATTCTCAAGGATTTATTTG 2324 2 1 1 | Qy 526 | Oy 526 Sill Oy 526 Sill Oy 526 Sill Oy 526 Sill Oy 526 Oy 539 Oy 557 Oy 557 Oy 557 Oy 557 Oy 557 Oy 577 |
 | ATTTCTTTGCCTAT 2264 AGTTTCTTTGCCTAT 2264 ATTTCTTTTGCCTAT 2264 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTTGCCTAT 2264 Qy 539 ATTTCTTTTGCCTAT 2264 Qy 539 Db 1633 CTGGTTCAACACCC 2207 SpMetTrpGlyArg 273 :: | ATTGGTGGAGTAGA 2168 Db 1693 Qy 539 Db 1633 Db 1633 Db 1633 Db 1582 Qy 557 Qy 577 Db 1584 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 ATTTCTTTGCCTAT 2225 ATTTCTTTGCCTAT 2264 Oy 539 ATTTCTTTCACACCC 2207 SpMetTrpGlyArg 273 H H H H Oy 577 SpMetTrpGlyArg 273 H H H H Oy 597 ON 597
 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | hrPheGluGluIle 233 hrPheGluGluIle 233 hrPheGluGluIle 233 Db 1633

 | hrPheGluGluIle 233 | hrPheGluGluIle 233 Qy 539 | TASSILENTYTSETLENTHIVALPTOPHEGLYGINLYSPTOASSILEASPVAL 293 Db 1525 Db 1525 TANGETVALASSILEASPVAL 293 Db 1525 Db 1525 Db 1525 Db 1525 Db 1525
 | TASSILEUTYTSETLEUTHTVALPTOPHEGIYGINLYSPTOASILEASPVAI 293 | TASSILEUTYTSETLEUTHTVALPTOPHEGLYGLILYSPTOASSILEASPVAL 293 Db 1525 Db 1525 TASSILEUTYTSETLEUTHTVALPTOPHEGLYGLILYSPTOASSILEASPVAL 293 Db 1525 APTITION TO THE STANDARD AND AND AND AND AND AND AND AND AND AN
 | TASHLEUTYTSETLEUTHTVALPTOPHEGIYGINLYSPTOASHIEASPVAI 293 Db 1525 TASHLEUTYTSETLEUTHTVALPTOPHEGIYGINLYSPTOASHIEASPVAI 293 Db 1525 TASHLEUTYTSETLEUTHTVALPTOPHEGIYGINLANDAGATTTTA 2132 Db 1525 TASHLEUTYTSETLEUTHTVALPTOPHEGIYGINLANDAGATTTA 2132 Qy 615 TASHLEUTYTSETLEUTHTVALPTOPHEGIYGINLANDAGATTTA 2132 Db 1492 | TASSILEUTYTSETLEUTHTVALPTOPHEGIYGINLYSPTOASSITLEASPVAL 293 | TASSILEUTYTSGTLEUTHTVALPTOPHEGIYGINLYSPTOASJILEASPVAI 293 | TASSIL-EUTYTSETLEUTHTValProPheGlyGlnLysProAssIleAspVal 293 Db 1525 | TASSILEUTYTSETLEUTHTVALPTOPHEGIYGINLYSPTOASSITLEASPVAL 293 Db 1525 LAMETVALASPGINALATTPASPALAGINATGILEPHELYSGINATACTTGGATTTA 2132 Qy 615 JATTT
 | TASSILEUTYTSETLEUTHTVALPTOPHEGIYGINLYSPTOASJILEASPVAL 293 | TASSILEUTYTSETLEUTHTVALPTOPHEGLYGLINLYSPTOASSILEASPVAL 293 Db 1525 |
 | | TASSILEUTYTSETLEUTHTVALPTOPHEGLYGLINLYSPTOASSITLEASPVAL 293 Db 1525 | | TASSILEUTYTSETLEUTHTVALFTOPHEGLYGINLYSPTOASTIEARDVAL 293 |
| TTGGTGAATCTAATGAAACGTTA 2435 TTGGTGAATCTGAACGTTA 2435 QY 486TyrGluGluTyr 183 QA 486 yrGluAspTyrGlyAspTyrTrp 203 :: Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :: Qy 506 alAsp | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 486 1735 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: Qy 506 1717GATTCTCAAGGATTTATTTGG 2324 AlAsp | Qy 486 | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 YICHASPTYICLYASPTYTTP 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 Y::: | GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: | GATTCTCAAGGATTTATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 Qy 526 alAsp | |
 | GATTCTCAAGGATTTATTTGG 2324 GATTCTCAAGGATTTATTTTGG 2324 213 | GATTCTCAAGGATTTATTTG 2324 alAsp | Qy 526 Salar Sal | Alasp | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPHEGIUGILE 233
 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 hrPheGluGluIle 233 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 PhrPheGluGluIle 233 ATTTCTTTGCCTAT 2264 Qy 539 ATTGGTGAGAGA 2168 Db 1633 Db 1582 CTGGTTCAACACCC 2207 SPMetTrpGlyArg 273 :: | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633
 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 hrPheGluGluIle 233 Db 1633 | hrPheGluGluIle 233 hrPheGluGluIle 233 Db 1633

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| TTGGTGAATCTAATGAAACGTTA 2435 TTGGTGAATCTGAAACGTTA 2435 QY 486TyrGluGluTyr 183 GAGCAATCTCGTTAGAAGATGGA 2378 QY 506 yrGluAspTyrGlyAspTyrTrp 203 ::: | TTGGTGAARCTATTGAAACGTTA 2435 TyrGluGluTyr 183 ::: ::: | Qy 486 | Qy 486 GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 Qy 506 yrGluAspTyrGlyAspTyrTrp 203 :::

 | TyrGluGluTyr 183 | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 YIGLUASpTYGTLYSpTYTTP 203 ::: | GAGCAATCTCGTTAGAAGATGGA 2378 GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: |
 | GAGCAATCTCGTTAGAAGATGA 2378 GAGCAATCTCGTTAGAAGATGA 2378 QY 506 ;; -GATTCTCAAGGATTTATTTGG 2324 GATTCTCAAGGATTTATTTGG 2324 ALASP | GAGCAATCTCGTTAGAAGATGGA 2378 yrGluAspTyrGlyAspTyrTrp 203 ::: | | |
 | GATTCTCAAGGATTTATTTGG 2324 GATTCTCAAGGATTTATTTTGG 2324 213 :: :: TTGACCTGTATTTCTTTGCCTAT 2264 TTGACCTGTATTTCTTTGCCTAT 2264 Qy 539 alGluHisThrPheGluGluIle 233 TTTACCAT | GATTCTCAAGGATTTATTTG 2324GATTCTCAAGGATTTATTTG 2324 213 213 213 214 2264 227 2264 227 2264 227 238 247 257 261 261 261 277 287 287 287 287 287 287 287 287 287 | Qy 526 | Oy 526 Sill Oy 526 Oy 526 Oy 526 Oy 526 Oy 526 Oy 528 Oy 539 Oy 557 Oy | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 APPROCULTLE 233 APPROCULT 2225
CTASTALATYPPO 253 CTGGTTCAACACCC 2207 SPMEtTrpGlyArg 273 STATTGGTGGAGTAGA 2168 CASTILAASNIAL 206 COMMITTED | ATTTCTTTGCCTAT 2264 ATTTCTTTGCTGAGTAGA 2168 ATTTGGTGGAGTAGA 2168 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633 | ARTITCTTTGCCTAT 2264 ARTITCTTTGCCTAT 2264 Oy 539 hrPheGluGluIle 233 Db 1633 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Oy 539 hrPheGluGluIle 233 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 PARTHEGIUGILIE 233 ATTTCTTTGCCTAT 2264 QY 539 DD 1633 ATTTCTTCAACACCC 2207 ATTTCGTGCAGCTAGA 2168 ATTTCGTGCAGCTAGA 2168 QY 597 CASTICAASATAGA 2168 QY 597 | ATTTCTTTGCCTAT 2264 ATTTCTTTGCCTAT 2264 Qy 539 hrPheGluGluIle 233 Db 1633
 | hrPheGluGluIle 233 hrPheGluGluIle 233 Db 1633

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 | This:: :::::::::::::::::::::::::::::::::: | ::: | :: :: | | : : : :
 | | Db 1525 | |
 | | | Db cametValAspGlnalaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 partTr |
| \[\text{YTTTGCCGTATATGGTAGTCGCTGGTATTTTGGTGAACGTTA 2435} \] \[YSGInLeuArgProLeu | ###################################### | |

 | SGInLeuArgProLeu | | -ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAAGAGATGGA 2378 -ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAAGAAGATGGA 2378 | -ACAGGCTCGGACTCTGGATAAGGCAATCTCGTTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAATTTAGAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAATTAGAAAAATTAGAAAATTAGAAAATTAGAAAAATTAATTAGAAAAATTAAATTAGAAAAATTAAATTAGAAAATTAATTAGAAAAATTAAATTAGAAAAATTAAATTAGAAAAATTAAATTAGAAAAATTAAATTAAAATTAAAATTAAAATTAAAATTAAAA
 | ACAGGTTGGATAAGGCAGATGGAGGAATCTCGTTAAAAGAATGAGA 2378ACAGGTTCGGATAAGGCAGATGGAGGAATCTCGTTAAAAAGAATGAGAATGA 2378 | ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAGATGGA 2378 20194888761uMetAlaArgAlaAsnHiSTyrGluAspTyrGlyAspTyrTrp 203 20194887797GATTCTCAAGGATTTATTTGG 2324 202 | CCGAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTTATTTGG 2324 | | CCGAAAATGGTATAGCCTTATTGGATCATTCTCAAGGATTTATTTGG 2324 Db 1/1/ CCGAAAATGGTATAGCCTTATTGGAT
 | CCGAAATGGTATAGCCTTATTGGATGATTCTCAAAGGATTTATTTGG 2324 Cy 526 Cy 527 Cy 5 | CyaranicGrafacCCTTaTTGGAT:GATTCTCAAGGATTTATTTG 2324 | 9GIYASPTYrGluValAsnGlyValAsp0 | 29GlyAspTyrGluValAsnGlyValAsp | 1
 | 1693 | Db 1693 ATCTGGTTATATTGAGAGAAATCAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAATCAAATTGACCTGTATTTCTTTGCCTAT 2264 Qy 539 PTYrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 ITATAGAGGAGCAATCAGAGATTTTACCAT 2225 225 227 227 227 228 239 240 251 252 253 265 277 278 278 278 278 278 278 27 | ### ATCTGGTTATATTGAGAGAAAATCAAAATTGACCTGTATTTCTTTGCCTAT 2264 ################################### | ATCTGGTTATATTGAGAGAGAAATCAAATTGACCTGTATTTGCCTAT 2264 ATCTGGTTATATATTGAGAGAGAAAATCAAATTGACCTGTATTTGCCTAT 2264 Qy 539 PFTYTSErArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233
 | ATCTGGTTATATTGAGAGAGAAATGAAATTGACCTGTATTTTTTTGCCTAT 2264 23 23 23 24 27 23 24 27 27 27 27 27 27 27 | ### STATE OF THATALT GAGAGAAAT CAAAT TIGACCTGTATT TOTTTGCTAT 2264 | ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 Qy 539

 | pPTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 Qy 539 | ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 23 Qy 539 l |
 | | LDD 1323
 | 1225 | 1225 | | 1225 | 125
 | 1225 | 123 | 125
 | 1225 | 1223 | 125 | DD |
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 | | | -ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGAGATGGA 2378 -ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGAGATGGA 2378 -ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGAGATGGA 2378 | ACAGCTCGGATCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 Db 1735
 | ACAGGTTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378ACAGGTTCGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATTGA 2378 | ACAGCTCGGACTCTGGATAAGGCAATCGGAGATGGA 2378 | CCGAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTTATTTGG 2324 | | CONTROL CONT | CCGAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTTATTTGG 2324
 | Command Colling Collin | QgGlyAspTyrGluValAsnGlyValAspH | 23 Qy 526 11 < | 1 | 1693 AATCTGGTTATATTGAGAAAATCAAATTGACCTGTATTTCTTTGCCTAT 2264 2264 2264 2264 2264 2264 2264 2264 2264 2264 2264
2264 2264 2264 2264 2264 2264 2264 2264 2264 2264 2264 2264 2264 2265 | Db 1693 ATCTGGTTATATTGAGAGAGAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAATTGAACTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAATTGACCTGTATTTCTTTGCCTAT 2264 Qy 539 ppTyrSerArgGlyGlnLeuileGluAspValGluHisThrPheGluGluIle 233 | | ATCTGGTTATATTGAGAGAGAAATCAAATTGACCTGTATTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAAATCAAATTGACCTGTATTTGCCTAT 2264 Qy 539 PSPTYSEARGGIYGInLeuIleGluAspValGluHisThrPheGluGluIle 233 IIII | AATCTGGTTATATTGAGAGAGAAAATCAAATTGACCTGTATTTTTTTT
 | ### PROPERTY OF THE FAIR TO GAGARATE CAPATE GACCEG TATTECTTE GCTAT 2264 | ppTyrSerArgGJYGInLeuIleGluAspValGluHisThrPheGluGluIle 233 Qy 539

 | pPTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 Qy 539 |
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 | | | | | CONTRACT CONTRACT | Comparison of the control of the c | Comparison
 | CONTACTACGATTACGATTACACTTCGCATTACATTCCACCTCCC | CATTOM CONTINUES CONTINU | 2132 Qy 615 |
 |
| VITTTGCCGTATÀTGGTAGTCGCTGGTATTTGGTGAATCTTATGAATCTTA 2435 | ###################################### | |

 | SGInLeuArgProLeuTyrGluGluTyr 183 | | ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGAGATGGA 2378ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGAGATGGA 2378 20 | -ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 -ACAGCTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378
 | -ACAGGTTGGATAAGGCAGATGGAGCAATCTCGTTAAAAGATGGA 2378 -ACAGGTTCGGATAAGGCAGATGGAGCAATCTCGTTAAAAGAATGGA 2378 | ACAGCTCGGACTCTGGATAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 | 1 | | 1/1
 | CCGAAATGGTATAGCCTTATTGGATGATTCTCAAAGGATTTATTTGG 2324 232 | Oy 526 | QQIYASPTYRGluValAsnGlyValAspG | 79GlyAspTyrGluValAsnGlyValAsp
 | 1 | 1693 | Db 1693 ATCTGGTTATATTGAGAGAGAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAATTGAACTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAATTGAACCTGTATTTCTTTGCCTAT 2264 Qy 539 pTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 |
 | ATCTGGTTATATTGAGAGAGAAAATTGACCTGTATTTGCCTAT 2264 ATCTGGTTATTGAGAGAGAAAATTGACCTGTATTTGCCTAT 2264 Qy 539 PPTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | ATCTGGTTATATTGAGAGAGAAATTGACCTGTATTTTTTTT | ### 175 1 1 1 1 1 1 1 1 1 | 1 1 1 1 1 1 1 1 1 1

 | pTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 Qy 539 l | ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 Qy 539
 | |
 | LaMetValAspGlnalaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Qy 615 LaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db 1492 | COTTATACGTCGGATGAATACTTGGATTA 2132 Qy 615 LaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 | | | LaMetValAspGlnalaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db 1492 ATTTGAAACAGAGAAA 2108 Qy 627
 | | AmetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Qy 615 AmetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db 1492 AmetValGlyLeuProAsnMetGAAACAGAGAAA 2108 Qy 627 AmetValGlyLeuProAsnMet | COTTATACGTCGGATGAATACTTGGATTA 2132 Qy 615 Qy 627 | AmetValAspGlnalaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Qy 615 AmetValAspGlnalaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db 1492 AmetValAspGlnalaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db 1492 AmetValGlyLeuProAsnMet
 | AmetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Qy 615 | COTTATACGGGATGAATACTTGGATTA 2132 Qy 615 Qy 627 Qy | AmetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 | AMETVALASpGInAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 AMETTT |
| | ###################################### | |

 | SGInLeuArgProLeu | | ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 |
 | -ACAGGTTGGATAAGGCAGATGGAGGCAATCTCGTTAAGAGATGGA 2378 -ACAGGTTCGGATAAGGCAGATGGAGGCAATCTCGTTAAGAGATTGA 2378 | ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 201ysAsnGluMetAlaArgAlaAsnHiSTyrGluAspTyrGlyAspTyrTrp 203 201ysAsnGGluMetAlaArgAlaAsnHiSTyrGluAspTyrGlyAspTyrTrp 203 202GAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTTATTTGG 2324 203 | Db 1717 | | COCANANGGTATAGCCTTATTGGATGATTCTCAAGGATTTATTTGG
 | 10 10 10 10 10 10 10 10 | GGLyAspTyrGluValAsnGlyValAsp | QY 526 11 ::: :: :: :: :: :: ::: ::: ::: :::: ::::::: ::::::::::: :::::::::::::::::::::: :::::::::::::::::::::::::::::::::::: | 29GlyAspTyrGluValAsnGlyValAsp
 | | 1693 | Db 1693 ATCTGGTTATATTGAGAGAAATCAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAATCAAATTGACCTGTATTTCTTTGCCTAT 2264 Qy 539 pTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 |
 | ATCTGGTTATATTGAGAGAGAAATCAAATTGACCTGTATTTGCCTAT 2264 ATCTGGTTATATATTGAGAGAGAAAATCAAATTGACCTGTATTTGCTTTGCCTAT 2264 Qy 539 PFTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | ATCTGGTTATATTGAGAGAGAAATTGACCTGTATTTCTTTGCCTAT 2264 QY 539 pTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | ### 175 1977 | APTYTSERARGGLYGINLEWILLEGULASPVALGULII 23 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

 | pPTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 Qy 539 yTATAGAGGAGCAATCAGAGATTTTACCAT
 | ametValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 ph 1402 | Qy 615 LaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313
 | Qy 615 LaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 LATTT | AMETVALASpGlnalaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 | Qy 615 LaMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 | Qy 615 AMETVALASpGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 | Qy 615 AMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313
 | AmetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 | Qy 615 Qy 615 QY 617 QY 618 QY 619 QY 627 | Qy 615 AMetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 | AmetValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313
 | Qy 615 AMETVALASpGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db 1492 ATTT | AMETVALASpGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db 1492 ATTT | Qy 615 AMETVALASpGInalaTrpAspAlaGInArgIlePheLysGluAlaGluLys 313 | QY AMETVALASpGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313
 |
| WITTTGCCGTATÀTGGTAGTCGCTGGTAITTTGGTGAATCTAATGAAACGTTA 2435 /*SGInLeuArgProLeu | ###################################### | |

 | | | -ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGAGATGGA 2378 -ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGAGATGGA 2378 -ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGAGTGGA 2378 | -ACAGGCTCGGACTCTGGATAAGGCAATTGGAGGAATCTCGTTAGAAGATGGA 2378 -ACAGGCTCGGACTCTGGATAAGGCAATTGGAGGAATCTCGTTAGAAGATGGA 2378
 | -ACAGGTTGGATAAGGCAGATGGAGGAATCTCGTTAAGAGATGGA 2378 -ACAGGTTCGGATAAGGCAGATGGAGGAATCTCGTTAAGAGATTGA 2378 | ACAGCTCGGACTCTGGATAAGGCAATCTCGTTAGAAGATGGA 2378 | | | CGAAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTTATTTGG 2324 CGCGAAATGGTATAGCCCTTATTGGAT
 | CCGAAATGGTATAGCCTTATTGGATGATTCTCAAAGGATTTATTTGG 2324 Cy 526 | CyaranicGrafacCCTTATTGGATGATTCTCAAGGATTTATTTGG 2324 2326 | QgGlyAspTyrGluValAsnGlyValAsp0 | 9GlyAspTyrGluValAsnGlyValAsp
 | 1 | 1693 ATCTGGTTATATTGAGAAGAAAATCAAAATTGACCTGTATTTCTTTGCCTAT 2264 1 | ATCTGGTTATATTGAGAGAGAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAATTGAACTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAATTGAACTGAACTGTATTTCTTTTGCCTAT 2264 Qy 539 ppTyrSerArgGlyGlnLeuileGluAspValGluHisThrPheGluGluIle 233 |
 | ATCTGGTTATATTGAGAAGAAAATCAAATTGACCTGTATTTGCCTAT 2264 ATCTGGTTATATATTGAGAAGAAAATCAAATTGACCTGTATTTGCCTAT 2264 Qy 539 PPTYSErArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | ATCTGGTTATATTGAGAGAGAAAATGACCTGTATTTTGCCTAT 2264 ATCTGGTTATATATTGAGAGAGAAAATGACCTGTATTTTTTTT | ### PROPERTY OF THE PRINCE OF THE PROPERTY OF THE PRINCE OF THE PROPERTY OF TH | ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 Qy 539

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 | ValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 | ValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 | ValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 | ValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Qy 615 | Qy 615 ValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313
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| VITTTGCCGTATÀTGGTAGTCGCTGGTATTTGGTGAATCTTATTGAAGCTTA 2435 243 | ATTITICCGTANATGGTAGTCGCTGGANTTTGGTGAANCCTATA 2435 SGInLeuArgProLeuTyrGluGluTyr 183 | |

 | SGInLeuArgProLeuTyrGluGluTyr 183 | | ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGAGATGGA 2378ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGAGATGGA 2378 20 | -ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 -ACAGCTCGGACTCTGGATAAGGCAGATGGAGGCAATCTCGTTAGAAGATGGA 2378
 | -ACAGCTCGGACTCTGGATAAGGCAGATGGAGGAATCTCGTTAAAAGAATGGA 2378 -ACAGCTCGGACTCTGGATAAGGCAGATGGAGGAATCTCGTTAAAAAGAATGGA 2378 | ACAGCTCGGACTCTGGATAAGGCAATCTCGTTAGAAGATGGA 2378 | CCGAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTTATTTGG 2324 | Db 1717 CCCGAAATGGTATAGCCTTATTGGAATGATTCTCAAGGATTAATTTGG 2324 Db 1717 CCCGAAATGGTATAGCCTTATTTGGAATGATTCTCAAGGATTTAATTTGG 2324 Oy 526 GgGlyAapTyrGluValAsnGlyValAsp | COCCENTATIGGAT
 | CCGAAATGGTATAGCCTTATTGGATGATTCTCAAAGGATTTATTTGG 2324 Cy 526 | Oy 526 | QQ 526 1 <td>79GlyAspTyrGluValAsnGlyValAsp</td> <td> </td> <td> 1693 1 1 1 1 1 1 1 1 1 1</td> <td>ATCTGGTTATATTGAGAGAAAATCAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAAATCAAAATTGACCTGTATTTCTTTGCCTAT 2264 QY 539 ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 </td> <td> </td> <td>ATCTGGTTATATTGAGAGAGAAAATTGACCTGTATTTGCTTTGCCTAT 2264 ATTCTGGTTATTGAGAGAGAGAAAATTGACCTGTATTTGCTTTGCCTAT 2264 ATTCTGGTTATATTGAGAGAGAGAAAATTGACCTGTATTTTCTTTGCCTAT 2264 Qy 539 PTYTSETATGG1VG1nLeu11eG1uAspValG1uHisThrPheG1uG1uIle 233 IIII</td> <td>ATCTGGTTATATTGAGAGAGAAATGACATTGACCTGTATTTCTTTGCCTAT 2264 Qy 539 ppTyrSerArgGlyGlnLeuileGluAspValGluHisThrPheGluGluIle 233 </td> <td>### PROTEST AND THE ANALYTICA AND THE ANALYTICATE CONTROLLED TO THE ANALYTICA AND THE ANALYTICA AND THE ANALYTICATE CONTROLLED TO THE ANALYTICATE CONTROLLED</td> <td> 1 </td> <td>pTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 Qy 539 l </td> <td>ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 Qy 539 </td> <td>313</td> <td>ValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 27 27 27 28 28 29 29 20 20 20 20 20 20 20 20 20 20 20 20 20</td> <td>ValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db 1492</td> <td>ValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313</td> <td>ValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 </td> <td>ValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 </td> <td>ValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 </td> <td>ValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 </td> <td>313 Db 1492
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 | ATCTGGTTATATTGAGAGAGAAATGACATTGACCTGTATTTCTTTGCCTAT 2264 Qy 539 ppTyrSerArgGlyGlnLeuileGluAspValGluHisThrPheGluGluIle 233 | ### PROTEST AND THE ANALYTICA AND THE ANALYTICATE CONTROLLED TO THE ANALYTICA AND THE ANALYTICA AND THE ANALYTICATE CONTROLLED TO THE ANALYTICATE CONTROLLED | 1

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 | ValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 27 27 27 28 28 29 29 20 20 20 20 20 20 20 20 20 20 20 20 20 | ValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313 Db 1492 | ValAspGlnAlaTrpAspAlaGlnArgIlePheLysGluAlaGluLys 313
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 | SGInLeuArgProLeuTyrGluGluTyr 183 | | ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 2011ysAsnGlumetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrp 203 | -ACAGGCTCGGACTCTGGATAAGGCAATCTCGGTTAGAAAAAAAA
 | -ACAGGTTGGATAAGGCAGATGGAGGAATCTCGTTAAAAGAATGGA 2378 -ACAGGTTCGGATAAGGCAATCTCGTTAAAAGAATGGA 2378 | ACAGCTCGGACTCTGGATAAGGCAGATGGAGATGGAAGATGGA 2378 201ysAsnGluMetAlaArgAlaAsnH1STyrGluAspTyrGlyAspTyrTrp 203 203 203 204 205 207 208 208 209 208 209 208 209 208 209 208 209 208 209 208 209 208 209 208 209 208 209 208 209 209 | | | SCGAAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTTATTTGG 2324 CYSCGAAAATGGTATAGCCTTATTGGAT
 | CCGAAATGGTATAGCCTTATTGGATGATTCTCAAAGGATTTATTTGG 2324 232 | Oy 526 | QglyAspTyrGluValAsnGlyValAspC | 79GlyAspTyrGluValAsnGlyValAsp
 | | 1693 | Db 1693 ATCTGGTTATATTGAGAGAAATCAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAATCAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAAATCAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAAATCAAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAATTTTTACCAT | ATCTGGTTATATTGAGAGAAAATCAAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTTGAGAGAGAAAATCAAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAAATCAAAATTGACCTGTATTTCTTTTGCCTAT 2264 AY 539 PTYYSErArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 ATTATAGAGGAGCAATCAGAGATTTTTACCAT
 | ATTCTGGTTATATTGAGAGAGAAAATCAAATTGACTTGTTTGCCTAT 2264 ATTCTGGTTATATTGAGAGAGAAAAATCAAATTGACTTGTTTGCCTAT 2264 Qy 539 PPTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | ATCTGGTTATATTGAGAGAGAAATGACATTGACCTGTATTTCTTTGCCTAT 2264 QY 539 pTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | ### PROPERTY OF THE PROPERTY O | 1 1 1 1 1 1 1 1 1 1

 | pPTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 Qy 539 1 1 1 | 313
 | VALASPGINALETPASPALAGINARGILEPNELYSGLUALAGINLYS 313 Db 1492 | valaspelnalatrpaspalaGinargilePheLysGilalaGildys 313 Db 1492
 | VOLASPGIDATSTEPASPALAGIDATSTICEPNELYSGIDALAGIDLYS 313 GAAACAGAGAAA 2108 Db 1492 | VALASPGINALETTPASPALEGINATGILEPNELYSGIUALEGIULYS 313 | VALASPGINALATTPASPALAGINATGILEPNELLYSGINALAGINLYS 313 | VALASPGIDALBUTPASPALAGIDATGILEPNELLYSGIDALBGIDLYS 313 Db 1492 GAAACAGAGAAA 2108 Qy 627 | ValaspulnatarrpaspalaGinargilePhelysGluAlaGlubys 313 Db 1492 GADACAGAGAAA 2108 Qy 627 ValGlufenBroAsnMatrussess Qy 627
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 | SGInLeuArgProLeu | | -ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 -ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 20 | -ACAGGCTCGGACTCTGGATAAGGCAATCTCGTTAGAAAATTAGAAAATTGAA 2378 -ACAGGCTCGGACTCTGGATAAGGCAATCTCGTTAGAAAAATTAGAAAATTGAAAAATTGATTTGA 2378
 | | ACAGCTCGGACTCTGGATAAGGCAGATGGAGATGTAGAAGATGGA 2378 | | | CCGAAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTTATTTGG 2324
2324 232 | CCGAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTTATTTGG 2324 | CGAMANGCCTTATTGGAT:GATTCTCAAGGATTTATTTG 2324 23 23 23 23 24 25 25 25 25 25 25 25 | 9GIYASPTYrGluValAsnGlyValAsp0 | 29GlyAspTyrGluValAsnGlyValAsp
 | 1 | 1693 | Db 1693 ATCTGGTTATATTGAGAGAAAATCAAAATTGACCTGTATTTCTTTGCCTAT 2264 Qy 539 pTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | ATCTGGTTATATTGAGAGAGAAATCAAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTTGAGAGAGAAAATCAAAATTGACCTGTATTTCTTTGCCTAT 2264 Qy 539 ppTyrSerArgGlyGlnLeuileGluAspValGluHisThrPheGluGluIle 233
 | ATCTGGTTATATTGAGAGAGAAATCAAATTGACCTGTATTTGCCTAT 2264 ATTCTGGTTATATTGAGAGAGAAAATCAAATTGACCTGTATTTGCCTAT 2264 Qy 539 PFTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | AATCTGGTTATATTGAGAGAGAAAATGACATATTGACCTGTATTTTTTTT | ### PROPERTY OF THE FAT TO GAGARA TO GAGAT TO GA | 1 1 1 1 1 1 1 1 1 1

 | pPTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 23 | ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 Qy 539 | 0 H 1 M 1 M 1 M 1 M 1 M 1 M 1 M 1 M 1 M 1
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 | SGInLeuArgProLeuTyrGluGluTyr 183 | | ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGAGTGGA 2378ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGAGTGGA 2378 | -ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 -ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378
 | -ACAGGTTGGATAAGGCAGATGGAGGAATCTCGTTAGAAGATGGA 2378 -ACAGGTTCGGATAAGGCAGATGGAGGAATCTCGTTAGAAGATGGA 2378 | ACAGCTCGGACTCTGGATAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 201ysAsnGluMetalaArgAlaAsnHisTyrGluAspTyrGlyAspTyrTrp 203 203 204 205 207 208 209 209 209 201 209 201 201 201 | | | COCCENTATIGGAT
 | CCGAAATGGTATAGCCTTATTGGATGATTCTCAAGGATTTATTTGG 2324 | Oy 526 | QgGlyAspTyrGluValAsnGlyValAspT | QglyAspTyrGluValAsnGlyValAsp
 | 1 | 1693 APTCTGGTTATATTGAGAAAATCAAATTGACCTGTATTTGCCTAT 2264 2265 226 | Db 1693 ATCTGGTTATATTGAGAGAGAAATCAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAATCAAATTGACCTGTATTTCTTTGCCTAT 2264 Qy 539 ppTyrSerArgGlyGlnLeuileGluAspValGluHisThrPheGluGluIle 233 |
 | ATCTGGTTATATTGAGAGAGAAATCAAATTGAACTGTATTTGCTTTGCCTAT 2264 ATTCTGGTTATATTGAGAGAGAAAATCAAATTGAACTGTATTTGCTTTTGCCTAT 2264 23 ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 23 | ATCTGGTTATATTGAGAGAGAAATGACATTGACCTGTATTTTTTTT | ### CIPS TIALATI GAGAGAAAT CAAAT TIGACCIG TATTICCTTT 2264 QY 539 ### STYTS STATE OF THE COLOR | 1

 | pPTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | 7 1/02
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| YSGInLeuArgProLeu | ###################################### | |

 | SGInLeuArgProLeuTyrGluGluTyr 183 | | ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 20 21 | -ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 -Db 1735 -DcGAAATGGTATAGCCTTATTGGAT
 | -ACAGGTTGGATAAGGCAGATGGAGCAATCTCGTTAAAAGATGGA 2378 -ACAGGTTCGGATAAGGCAGATGGAGCAATCTCGTTAAAAAGATGGA 2378 | ACAGCTCGGACTCTGGATAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 | | | COCANATGGTATAGCCTTATTGGAT
 | 1 1 1 1 1 1 1 1 1 1 | Oy 526 | QQLYASPTYRGLUVBLASGLYVBLASGLYVBLASGLYVBLASGLYVBLASGLYVBLASGLYVBLASGLYVBLASGLYVBLASGLYVBLASGLYVBLASGLYVBLASGLYBBLAS | 79GlyAspTyrGluValAsnGlyValAsp
 | | 1693 | ATCTGGTTATATTGAGAGAGAAATCAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAAATCAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAATCAAAATTGACCTGTATTTCTTTGCCTAT 2264 QY 539 PTYSEARTGGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 IIII | ### ATCTGGTTATATTGAGAGAGAAAATCAAAATTGACCTGTATTTCTTTGCCTAT 2264 ################################## |
ATCTGGTTATATTGAGAGAGAAAATCAAATTCAAATTCAAATTGACTTTTGCCTAT 2264 ATTCTGGTTATATTGAGAGAGAGAAAATCAAATTCAAATTCATTTTTTTT | ATCTGGTTATATTGAGAGAGAAATGACATTGACCTGTATTTTTTTGCCTAT 2264 QY 539 ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | ### PROPERTY OF THE PROPERTY O | 1 1 1 1 1 1 1 1 1 1

 | pTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 Qy 539 l | ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 |
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 | SGInLeuArgProLeu | | ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 | -ACAGGCTCGGACTCTGGATAAGGCAATTGGAGGCAATCTCGTTAGAAAATGGA 2378
 | -ACAGGTTGGATTAAGGCAGATGGAGCAATCTCGTTAAAAAGATGGA 2378 -ACAGGTTCGGATAAGGCAGATGGAGCAATCTCGTTAAAAAAAA | ACAGCTCGGACTCTGGATAAGGCAGATGGAGCAATCTCGTTAGAAGATGGA 2378 201493ASTGGLUMETALAATGALAASTHISTYTGLUASPTYTTYP 203 20141 | 1 | | COGNAMATGGTATAGCCTTATTGGAT
 | 100 100 | Oy 526 | QgGlyAspTyrGluValAsnGlyValAsp | 29GlyAspTyrGluValAsnGlyValAsp
 | | 1693 | Db 1693 ATCTGGTTATATTGAGAGAAATCAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAATCAAATTGACCTGTATTTCTTTGCCTAT 2264 Qy 539 pTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | ATCTGGTTATATTGAGAGAAAATCAAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAAATCAAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAAATCAAAATTGACCTGTATTTCTTTGCCTAT 2264 ATCTGGTTATATTGAGAGAGAAAATCAAAATTGACCTGTATTTTCTTTGCCTAT 2264 ATTATAGAGGAGCAATCAGAGATTTTTACCAT
 | ATCTGGTTATATTGAGAGAGAAATCAAATTGACCTGTATTTGCCTAT 2264 ATCTGGTTATATATTGAGAGAGAAAATCAAATTGACCTGTATTTGCCTAT 2264 ATTATAGAGGAGCAATCAAATTTTACCAT | ATCTGGTTATATTGAGAGAGAAATGACATTGACCTGTATTTTTTTGCCTAT 2264 ATCTGGTTATATTTGAGAGAGAAAATGACATTGACCTGTATTTTTTTT | ### PROPERTY OF THE FATE FOR AGAAAST CAAAST CAAAAST CAAAAST CAAAAST CAAAAST CAAAAST CAAAAST CAAAAST CAAAAST CAAAAAST CAAAAAST CAAAAAST CAAAAAAAAAA | ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233

 | pPTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 | ppTyrSerArgGlyGlnLeuIleGluAspValGluHisThrPheGluGluIle 233 Qy 539 | - 4 - 1
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 | ValGluTenDroAsnMetQy 627 | 2108 Qy 627
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alAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsnGlnMetIle 663		lalenCludenIvsBlaTurCluTrpBenBenBenCluMo+TurIonDhoBraCorCor	 	gIleSerLeuLys		pserThrAspTrpSe	TATAGTTGG	LysAsnMetAsnValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLys 5	TCCTTAAGATTTCAACCCTATTTTACAGCGACAGCATCTAATATCGGT	uArgLeuGlyLysSerGluProTrpThr	AGTCACCGCTACCCTGTTGGTTTTTCAGGGGATACTATTATTAGTTGGAAT	isLysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAs	CAGGATAGTTGTAAAAATGCAGAAGGTGGTTTGATTTTATCAAGATATGCAGGTCCTGGT 1	lnGluAlaLeuCysGlnAla	::: TGGCTTTTAAACCATTATCACTAT	ValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeuTyrGlnPheGlnPhe 5	GGTATGCTAGATCCACTT	GlyValValGluproValProHisAspGluThrTyrCysAspProAlaSerLeuPheHis 5		sLysTrpTrpGluMetLys <i>t</i>	TATGAACTAGAAAAG	ValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArgTrpMetValPheLysGly 4	TCTTTTAGGGAAGCCTACTTTAAAGATGTTCAT	AspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeuLysGlnAlaLeuThrIle 4	TTTTT	lleGlyLeu		Eeu	CGGGCTTATGAAGAAGCTTAT	MetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGlu	TA	uThrAlaHisHisGluMetGlyHis	TTATTGCAACAACTTCATGATAGAAAGCTAAAAACTCTCC	gIle	TTTGGAAGTGGCTGGACAGGATATAGTTGGAATAGAAACTTAATACCAAATCCAGAACAG	
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Db 1372 ACATCTAAGATTATGAAGAAATAC---CTTCGTTTGAGACATCAGATGATT 1325

Search completed: March 7, 2003, 09:50:13 Job time : 166 secs

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Command line parameters:

MODEL-frame+_p2n.model -DEV=xlp

-MODEL-frame+_p2n.model -DEV=xlp

-Q-cgn2_1/USPTO_Spool/US09978385/runat_28022003_104718_1445/app_query.fasta_1.967

-DB-Published_Applications_NA -QFWT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1

LOOPECL-0 -LOOPEXT-0 -UNITS-blts -START-1 -RND--1 -MATRIX=blosum62

-TRANS-human40.cdd -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100

-THR_MIN-0 -ALIGN-20 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0

-MAXLEN-200000000 -USER-US09978385_@CGN_1_1_80_@runat_28022003_104718_1445

-NCPU-6 -ICPU-3 -NO_XLEXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG

-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT-7 -YGAPOP=10 -YGAPPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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3325
3732
3732
  US-09-978-385-1
US-10-114-893-85
US-10-028-072-71
US-10-121-049-71
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Sequence 1, Appli
Sequence 85, Appl
Sequence 71, Appl
Sequence 71, Appl
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ALIGNMENTS

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US-09-978-385-1
US-09-978-385-1
Sequence 1, Application US/09978385
Patent NO. US20020177211A1
GENERAL INFORMATION:
APPLICANT: Piddington, Christopher S.
APPLICANT: Piddington, Christopher S.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
FILE REFERENCE: 99-24C1
CURRENT APPLICATION NUMBER: US/09/978,385
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/133,952
PRIOR APPLICATION NUMBER: 60/133,952
PRIOR APPLICATION NUMBER: 60/151,181
PRIOR APPLICATION NUMBER: 09/2563,516
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 09/563,516
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 3334
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (35)...(2449)
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318

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APPLICANT: McCoy, John M.

APPLICANT: McCoy, John M.

APPLICANT: McCoy, John M.

APPLICANT: Collins-Racie, Lisa A.

APPLICANT: Collins-Racie, Lisa A.

APPLICANT: Evans, Cheryl

APPLICANT: Treacy, Maurice

APPLICANT: Bowman, McChael R.

APPLICANT: Spaulding, Vikki

APPLICANT: Spaulding, Vikki

APPLICANT: Spaulding, Vikki

APPLICANT: Genetics Institute, Inc.

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

FILE REFERENCE: GI 6000-10A

CURRENT APPLICATION NUMBER: US/10/114,893

CURRENT APPLICATION NUMBER: US/10/114,893

CURRENT FILING DATE: 2002-04-02

EARLIER FILING DATE: 1999-10-06

NUMBER OF SEQ ID NOS: 321

SOFTMARE: Patentin Ver. 2.0
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                                                                                                                                                                                               TYPE: DNA
ORGANISM: HOMO
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Matches:
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           CysThrLysValThrmetAspAspPheLeuThrAlaHisHisGlumetGlyHisILeGln
                                                                                                       TGCACAAAGGTGACAATGGAGGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAG
                                                              LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet
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                                                   AAAGCAGTCTGCCATCCCACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATG
                                                                                                                                                              AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu
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                                                                                                                             GlnMetIleLeuPheGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSer
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Publication No. US20030004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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CURRENT FILING DATE: 2001-12-19
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OR FILING DATE: 1997-06-18
OR APPLICATION NUMBER: 60/056974
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OR APPLICATION NUMBER: 60/059113
OR FILING DATE: 1997-09-17
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Filvaroff, Ellen
Gao, Wei-Qiang
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Sherwood, Steven
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APPLICATION NUMBER: 60/063561 FILING APPLICATION NUMBER: 60/064809 FILING DATE: 1997-11-07 APPLICATION NUMBER: 60/064248 FILING DATE: 1997-11-03 APPLICATION NUMBER: FILING DATE: 1997-10-28
APPLICATION NUMBER: 60/063704
FILING DATE: 1997-10-29 APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: 60/063329 FILING DATE: APPLICATION NUMBER: 60/063327 APPLICATION NUMBER: 60/063127 FILING DATE: 1997-10-24 APPLICATION NUMBER: FILING DATE: 1997-10 FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063045
FILING DATE: 1997-10-24 DATE: : 1997-11-17 1998-03-27 1998-03-20 1998-02-27 1998-03-25 1998-02-09 1998-02-04 1997-12-11 1997-10-27 1997-10-31 1998-01-23 1997-11-24 1997-10-60/081229 60/081203 60/080165 60/079294 60/074092 60/072320 60/069694 60/065186 60/079663 60/078910 60/077791 60/074086 60/073612 60/069334 60/066511 60/063733 60/063550 60/063082

PRIOR PRIOR OR APPLICATION NUMBER: 60/087106
OR APPLICATION NUMBER: 60/087106
OR APPLICATION NUMBER: 60/088026
OR APPLICATION NUMBER: 60/088026
OR APPLICATION NUMBER: 60/088730
OR APPLICATION NUMBER: 60/088741
OR APPLICATION NUMBER: 60/088741
OR APPLICATION NUMBER: 60/088810
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088810
OR APPLICATION NUMBER: 60/088810
OR APPLICATION NUMBER: 60/088858
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/089532
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089532
OR APPLICATION NUMBER: 60/089539
OR APPLICATION NUMBER: 60/089539 R APPLICATION NUMBER: 60/08

OR AFFLING DATE: 1998-05-07

OR AFFLING DATE: 1998-05-12

OR APPLICATION NUMBER: 60/08

OR FILING DATE: 1998-05-13

OR APPLICATION NUMBER: 60/0

OR FILING DATE: 1998-05-13 R FILING DATE: 1998-06-1
R APPLICATION NUMBER: 60,
R FILING DATE: 1998-06-2
DR APPLICATION NUMBER: 60,
R FILING DATE: 1998-06-2 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/091360 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091519 APPLICATION NUMBER: 60/090863 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 FILING DATE: 1998-0
APPLICATION NUMBER: FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089907 APPLICATION NUMBER: 60/085704 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085697 FILING DATE: 1998-05-15 FILLING DATE: 1998-05-13
APPLICATION NUMBER: 60/085339
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085579 APPLICATION NUMBER: 60/086430 APPLICATION NUMBER: FILING DATE: 1998-05 FILING DATE: 1998-05-FILING DATE: FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084627 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 APPLICATION NUMBER: 6 FILING DATE: 1998-04-APPLICATION NUMBER: FILING DATE: 1998-0 FILING DATE: 1998-04-APPLICATION NUMBER: 6
FILING DATE: 1998-04-APPLICATION NUMBER: 60/081695 FILING DATE: 1998-04-14 APPLICATION NUMBER: 60/084637 APPLICATION NUMBER: FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083545 1998-05-07 1998-06-23 1998-06-18 1998-05-22 1998-05-07 1998-06-19 1998-04-60/090538 60/090429 60/090349 60/089947 60/086414 60/085338 60/085323 60/085149 60/082999 60/081818 60/081817

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TrhrelyLysValCysAsnProAspAsnProGlnGlu	Matches: 802 Conservative: 1 Mismatches: 138 Indels: 2 Indels: 2 Gaps: 138 Gaps: 1 D72-71 (1-3732) SerLeuvalAlavalThrAlaAlaGlnSerThr	ngth: 3

A 2078	GTCAAAGAGAAGAAACCATAGATCATAGATGTAAATATATGTACATCTGGAACCCCTCA	2019	ф
555		555	Qy
A 2018	GGTGGAATATATCTGTTAATATGCATTCTTTTCTTATCTGCCAGAAGCAAATTTAGCCAA	1959	Db
- 555		555	Qу
G 1958	TTCTCCCTATCATAACTACAGCCCTCTCTTCCTGGTAATTGGAAGGAA	1899	Дb
- 555		555	Qy
T 1898	CATTTAATTTGTGGTCAGACAGGAACCTAGACCATACAACAATTGGGTGGG	1839	ф
- 555		555	Qy
A 1838	ATTTCTTTGTTCTAAAAAGAAAATTTTATGGCCTCAAAATGTCCTCATTTACAAACCAAA	1779	Дb
- 555		555	Qy
g 1778	AAATGTTGAACCTCTCCTAGTATTCAGTATTACTCATTTCCATGCCTAGGTTTGTATTTG	1719	Db
- 555		555	Qy
A 1718	GTGACATCTCAAACTCTACAGAAGCTGGACAGAAACTGTT-GTAAGAAATACCTC	1660	Db
- 555	LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuPhe	541	Qy
c 1659	GTCAAGCAGCTAAACATGAAGGCCC	1600	Db
s 540	yrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluG	521	Qy
r 1599	TGATGATTACTCATTCATTCGATATTACACAAGGACCCT	1540	Db
ս 520	laSerLeuPheHisValSerAsnAspTyrSerPheIleArgT	501	Qy
1539	GAGAGATAGTTGGGGTGGTGGAACCTGTGCCCCATGATGAAACAT	1480	Дb
500	ArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAsp	481	Qy
14	GTCTTTAAAGGGGAAATTCCCAAAGACCAG	N C	Db 47
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14	AGCACTCACGATTGTTGGGGACTCTGCCATTTACATGTTAGAC	6 4	Db 43
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1 1299	HisGluAlaValGJyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 	401 1240	Qy Db
12	ATGATATGGCATATGCTGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGA	1180	Db
40	TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe	381	Qy
1179	GCACAAAGGTGACAATGGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCC	1120	Db
380	ThrLysValThrMet	361	Qy
3 1119	AAAGCAGTCTGCCATCCCACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATG	1060	DЬ
360	LysAlaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet	341	Qy
1059	CCTAATATGACTCAAGGATTCTGGGAAAATTTCCATGCTAACGGACCCAGGAAATGTTCAG	1000	Db
340	ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln	321	Qy

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RESULT 4
US-10-121-049-71
GENERAL INFORMATION:
APPLICANT: Baker, Kevi
APPLICANT: Beresini,
APPLICANT: DeForge,
APPLICANT: Desovyers
APPLICANT: Desovyers
APPLICANT: Gao, Wei-
APPLICANT: Gao, Wei-
APPLICANT: Gerritser
APPLICANT: Goddard, APPLICANT: Godowski,
APPLICANT: Godowski,
APPLICANT: Gurney, Au
APPLICANT: Smith, Vic
                                                                                                                                                                                             Sequence 71, Application US/10121049 Publication No. US20030022239A1
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              Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                                  Baker, Kevin P.
                                                                                      Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
                                                                                                                                     DeForge, Laura
                                                                                                                                                    Beresini, Maureen
   Smith, Victoria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Watanabe,Colin K
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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                                                                                                          GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly
                                                                                                                                                                 ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr
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 GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu
                               GATTATTGGAGAGAGACTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGC
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                                                                                          GAAGAGTATGTGGTCTTGAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGG
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Qy 80 Db 285	27	Qу 74 Db 267	Qy 7 Db 26	Qy 7 Db 25	Qy 68 Db 249	Qy 66 Db 243	Qy 64 Db 237	Qy 625 Db 2318	Оу 606 Db 2258	Qy 586 Db 2198	Оу 566 Db 2139	ФУ 5 рь 20		0y 5		ОУ 5 Db 18	<u> </u>	Db 17
98 TATTAGCAAAGGAAAATAATCCAGGATTCCAAAACACTGATGATGTTCAGACCTCCTT 2857 05 e 805 - 58 T 2858	eArgAspArgLysLysLysAsnLysAlaArgSerGlyGluAsnProTyrAlaSerIleAs	5 1PheG 8 TTTTG	725 uGlyTleGlnProThrLeuGlyProProAsnGlnProProValSerIleTrpLeuIleVa 745 	05 gMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLe 725 	685 lThràlaProLysasnValSerAspIleIleProArgThrGluValGluLysAlaIleAr 705 	65 eGlyGluGluAspValArgValAlaAsnLeuLysProArgIleSerPheAsnPhePheVa 685 	645 rSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsnGlnMetIleLeuPh 665 	625 sSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSe 645 	606 TrpSerThrAspTrpSerProTyrAlaAsp-GlnSerIleLysValArgIleSerLeuLy 625 	586 AsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLysAsnSerPheValGly 605 	566 TrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsnValArgProLeuLeu 585 	556	GTCAAAGAGAAGAAACCATAGATCATAGATGTAAATATATGTACATCTGGAACCCCTCAA 20	959 GGTGGAATATATCTGTTAATATGCATTCTTTTCTTATCTGCCAGAAGCAAATTTAGCCAA 2018	555	555	39 CATTTAATTTGTGGTCAGACAGGAACCTAGACCATACAACAATTGGGTGGG	1779 ATTTCTTTGTTCTAAAAAGAAATTTTATGGCCTCAAAATGTCCTCATTTACAAACCAAA 1838

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RESULT 5 US-10-123-904-71

Sequence 71, Application US/101 Publication No. US20030022328A1

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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maured
APPLICANT: Desroyers, Laura
APPLICANT: Desroyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Goo, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin I
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Timothy
APPLICANT: Tumas, Daniel
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APPLICANT: Watanabe, Colin
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Best Local Similarity:
Query Match:
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; ORGANISM: Homo
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CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
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Gerritsen, Mary E.
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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                                  LysArgGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro
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                                 gMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLe
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LENGTH: 3732
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                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C160
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aLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSe 645 	ThrAspTrpSerProTyrAlaAsp-GlnSerIleLysValArgIleSerLeuLy 625	rPheGluProLeuPheThrTrpLeuLysAspGlnAsnLysAsnSerPheValGly 605 	rLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsnValArgProLeuLeu 585 		999 NGAGAAGAAACCATAGATCATAGATGTAAATATATGTACATCTGGAACCCCTCAA 2078	AATATATCTGTTÄATATGCATTCTTTTCTTATCTGCCAGAAGCAAATTTAGCCAA 2018	CTATCATAACTACAGCCCTCTCTTCCTGGTAATTGGAAGGAA	AATTTGTGGTCAGACAGGAACCTAGACCATACAACAATTGGGTGGG	555 TTTGTTCTAAAAAGAAATTTTATGGCCTCAAAATGTCCTCATTTACAAACCAAA 1838	TIGAACCICICCIAGIATICAGIATIACICAITICCAIGCCIAGGITIGIATITG 1778	PILeSerAsnSerThrGluAlaclyGlnLysLeuPhe	TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540 	rLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520 	gGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500 	tValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480 	nAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460 	yLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440 	AGCTGTTGGGGAAATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAAATCC 1299

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NUMBER OF SEQ ID NOS: 550
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CURRENT FILING DATE: 2002-06-19
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                                 CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu
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CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer
                                                                                                                  HisAlaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProILeGly
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              AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu
                                                                                                         TGCTTATTACTTGAACCAGGTTTGAATGAATAATGGCAAACAGTTTAGACTACAATGAG
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556AsnMetLeuArgLeuGlyLysSerGluPro 565	2019 GTCAAAGAGAAACCATAGATCATAGATGTAAATATATGTACATCTGGAACCCCTCAA 2078	555 555	959 GGTGGAATATATCTGTTAATATGCATTCTTTTCTTATCTGCCAGAAGCAAATTTAGCCAA 2018	555 555	.899 TTCTCCCTATCATAACTACAGCCCTCTCTTCCTGGTAATTGGAAGGAA	555 555	.839 CATTTAATTTGTGGTCAGACAGGAACCTAGACCATACAACAATTGGGTGGG	555 555	1779 ATTICITIGITCIAAAAAGAAAATTITAIGGCCTCAAAATGTCCTCAITTACAAACCAAA 1838	555 555	1719 AAATGTTGAACCTCTAGTATTCAGTATTACTCATTTCCATGCCTAGGTTTGTATTTG 1778	or remains a none and the second of the seco	541 LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuphe 555	521 TyrGlnPheGlnPheGlnAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis 540	1540 GCATCTCTGTTCCATGATTCTGATGATTACTCATTCGATATTACACAAGGACCCTT 1599	501 AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 520	481 LysargGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspPro 500	461 TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 480 	441 LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 460 	421 IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 440 	401 HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 420 	381 TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 400 	361 CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 380 	341 LysalaValCysHisProThralaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet 360 	321 ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln 340
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 71
LENGTH: 3732
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-918-71
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CURRENT APPLICATION NUMBER: US/10/176,918

CURRENT FILING DATE: 2002-06-20
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                                                          AspTyrTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGly 220
                                                                                                                   GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly
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555 1718	LysCysAspIleSerAsnSerThrGlualaGlyGlnLysLeuPhe		. Db
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520 1599	AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 		Qу
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480 1479	5GlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet 	N O	Qу
	laLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg 	6 4	Qy Db
440 1359	IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeuLeu 	421 1300	Qy Db
420 1299	HisGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 	401 1240	Qy Db
400 1239	TyrAspMetAlaTyrAlaAlaGlnProPheLeuLeuArgAsnGlyAlaAsnGluGlyPhe 	381 1180	Qy Db
380 1179	CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln 	361 1120	Qy
360 1119	LysalaValCysHisProThrAlaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet	341 1060	Оу
340 1059	ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln 	321 1000	Qy Db
320 999	AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 		Qy Db
300 939	LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln 	281 880	Qy Db
280 879	CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer 	261 820	Qy Db
260 819	HisalaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly	241 760	Qy Db
759	CAGTTGATTGAAGATGTGGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTT	700	Db

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                                                pIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAspValGlnThrSerPh 805
                                                                                                                     TTTTGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGAT
                                                                                                                                lPheGlyValValMetGlyValIleValValGlyIleValIleLeuIlePheThrGlyIl 765
                                                                                                                                                               gMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLe
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GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu
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                                                      CAGCAAAATGGGTCTTCAGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTA
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CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
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; ORGANISM: HOMO US-10-140-474-71
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APPLICANT:
                                                                LENGTH: 37
TYPE: DNA
                                                                                                        Prior Application removed - NUMBER OF SEQ ID NOS: 550
                                                                                                                                CURRENT FILING DATE: 2002-05-06
                                                                                                                                                          APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C162
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APPLICANT: Beresini, Maura
APPLICANT: DeForge, Laura
                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/140,474
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Wood, William
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APPLICANT: Baker, Kev.
APPLICANT: Beresini
APPLICANT: Deforge,
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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                                              Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Pred. No.:
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; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C251
; CURRENT APPLICATION NUMBER: US/10/142,431
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Payor Transmission of SEQ ID NOS: 550
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2797	2738 CAGAGATCGGAAGAAGAAAATAAAGCAAGAAGTGGAGAAAATCCTTATGCCTCCATCGA :	Db
785	ArgAspArgLysLysAsnLysAlaArgSerGlyGluAsnProTyrAlaSerIleAs	Qу
2737	2678 TTTTGGAGTTGTGATGGGATGATAGTGGTTGGGATTGTCATCTTGATCTTCACTGGGAT	Db
765	PheGlyValValMetGlyValIleValValGlyIleValIleLeuIlePheThrGlyIl	Qy
2677	2618 GGGGATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTTGT	Дb
745	GlyIleGlnProThrLeuGlyProProAsnGlnProProValSerIleTrpLeuIleVa	Qy
2617	2558 GATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCT	Db
725	MetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLe	Qy
2557	2498 CACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAG	Db
705	ThrAlaProLysAsnValSerAspIleIleProArgThrGluValGluLysAlaIleAr	Qy
2497	GGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGT	Dр
685	GlyGluGluAspValArgValAlaAsnLeuLysProArgIleSerPheAsnPhePheVa	Qγ
2437	CTTTT	DЬ
665	SerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsnGlnMetIleLeuPh	Qy
2377	2318 ATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATC	Db
645	SerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgSe	Qy
2317		Db
625	rpSerThrAspTrpSerProTyrAlaAsp-GlnSerIleLysValArgIleSerLeuLy	Qy
2257	2198 AACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTCTTTTGTGGGA	Db
605	snTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLysAsnSerPheValGly	Qy
2197	2139 TGGACCCTAGCATTGGAAAATGTTGTAGGAGC-AAGAACATGAATGTAAGGCCACTGCTC	рь
585	rpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsnValArgProLeuLeu	Qy
2138	2079 AAGGCCCTGAACCCCCTTTTTTTGTGTAGCAATATGCTGAGGCTTGGAAAATCAGAAACCC	DЬ
565	snMetLeuArgLeuGlyLysSerGluPro	Qу
2078	2019 GTCAAAGAGAAACCATAGATCATAGATGTAAATATATGTACATCTGGAACCCCTCAA	Дb
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2018	1959 GGTGGAATATATCTGTTAATATGCATTCTTTTCTTATCTGCCAGAAGCAAATTTAGCCAA	Дb
555	555	Qy
1958	1899 TTCTCCCTATCATAACTACAGCCCTCTCTTCCTGGTAATTGGAAGGAA	Дb
555	555	Qy
1898	1839 CATTTAATTTGTGGTCAGACAGGAACCTAGACCATACAACAATTGGGTGGG	Db
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C211
CURRENT APPLICATION NUMBER: US/10/143,114
CURRENT FILING DATE: 2002-05-09
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APPLICANT: Beresini, Mauro
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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                                                                                                                                                                                                                                                                                   CATGAAGCTGTTGGGGAAATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAAATCC
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uGlyIleGlnProThrLeuGlyProProAsnGlnProProValSerIleTrpLeuIleVa
                                                                                                gMetSerArgSerArgIleAsnAspAlaPheArgLeuAsnAspAsnSerLeuGluPheLe
                                                                                                                                                       CACTGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAG
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CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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TATCAAAGTTCACTTGCTTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAA
              TyrGlnSerSerLeuAlaSerTrpAsnTyrAsnThrAsnIleThrGluGluAsnValGln
                                                          ATTGAGGAACAGGCCAAGACTTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTC
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Godowski, Paul J.
Gurney, Austin L.
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Filvaroff, Ellen
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420	H1sGluAlaValGlyGluIleMetSerLeuSerAlaAlaThrPToLysHisLeuLysSer	401	DP QA
1299		1240	
400	TyraspMetalaTyralaalaGlnProPheLeuLeuArgasnGlyAlaasnGluGlyPhe	381	Qy
1239		1180	Db
380	CysThrLysValThrMetAspAspPheLeuThrAlaHisHisGluMetGlyHisIleGln	361	dq
1179		1120	qq
360 1119	LysalaValCysHisProThralaTrpAspLeuG1	341 1060	ФФ
340	ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAsnValGln	321	DP
1059		1000	OA
320	AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu	301	dd
999		940	88
300	LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln	281	da
939		880	Vo
280	CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer	261	Ф
879		820	
260 819	HisalaTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGly	241 760	pb Qy
240 759	GlnLeuIleGluAspValGluHisThrPheGluGluIleLysProLeuTyrGluHisLeu 	0 0	DP da
220	ASPTYTTIPATGG1YASPTYTG1uValASnG1YValASpG1YTYTASPTYTSeTATGG1Y	201	ФФ
699		640	
200	GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly	181 580	DP 6A
180	. ArgLeuTrpAlaTrpGluSerTrpArgSerGluValGlyLysGlnLeuArgProLeuTyr		DP
579			Ao
160	CysLeuLeuLeuGluProGlyLeuAsnGluIleMetAlaAsnSerLeuAspTyrAsnGlu	141	ф
519		460	
140 _.	AsnThrMetSerThrIleTyrSerThrGlyLysValCysAsnProAspAsnProGlnGlu	121	Db Qy
459		400	
120	GlnGlnAsnGlySerSerValLeuSerGluAspLysSerLysArgLeuAsnThrIleLeu	101	Db Qy
399		340	
100	GlnMetTyrProLeuGlnGluIleGlnAsnLeuThrValLysLeuGlnLeuGlnAlaLeu	81	Qy
339		280	Db
80	ASDMETASDASDA1AG1YASPLYSTIPSETA1APhELEULYSG1UG1DSETThTLEUA1A	61	ОУ
279		220	

alAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsnGlnMetIleLeuPh 665	rSerVal	645	Qy
CICTIGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATC 2377		2318	Db
aLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMetTyrLeuPheArgS	SerAla	625	Qy
ACCGACTGGAGTCCATATGCAGACCCAAAGCATCAAAGTGAGGATAAGCCTZ	TGGAGTA	2258	Db
ThrAspTrpSerProTyrAlaAsp-GlnSerIleLysValArgIleSerLe	rpSerT	606	Qy
TTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTCTTTTGTGGGA 2257	AACTACT	2198	Db
PheGluProLeuPheThrTrpLeuLysAspGlnAsnLysAsnSerPheValGl	TyrP	586	Qy
CTAGCATTGGAAAATGTTGTAGGAGC-AAGAACATGAATGTAAGGCCACTGCTC 2197	TGGACCC	2139	ДĎ
LeuAlaLeuGluAsnValYalGlyAlaLysAsnMetAsnValArgProLeuLe	rpThrL	566	ОУ
CTGAACCCCCTTTTTTGTGTAGCAATATGCTGAAGGCTTGGAAAATCAGAACCC 21	Geccc		D
AGAAGAAACCATAGATCATAGATGTAAATATATGTACATCTGGAACCCCTCA	GTCAAAG	2019	Db Db
555		555	Qy
AATATATCTGTTAATATGCATTCTTTTCTTATCTGCCAGAAGCAAATTTAGCCAA 2018	GGTGGAA	1959	Дb
555	1	555	Qy
CTATCATAACTACAGCCCTCTCTTCCTGGTAATTGGAAGGAA	TTCTCCC	1899	Дb
555		555	Qy
AATTTGTGGTCAGACAGGAACCTAGACCATACAACAATTGGGTGGG	CATTTAA	1839	ρb
555		555	Qy
ITTGTTCTAAAAAGAAATTTTATGGCCTCAAAATGTCCTCATTTACAAACCAAA 1838	ATTTCTT	1779	рb
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TTGAACCTCTCCTAGTATTCAGTATTACTCATTTCCATGCCTAGGTTTGTATTTG 1778	AAATGTT	1719	Db
555		555	Qy
ACATCTCAAACTCTACAGAAGCTGGACAGAAACT	AATGTO	1660	Db
AspIleSerAsnSerThrGluAlaGlyGlr	- 63	541	Qy
TTCCAGTTTCAAGAAGCACT	TACCAAT	1600	Db
PheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeu	rGlnÞ	521	Qy
	<u> </u>	1540	дb
euPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThr	laSerL	501	Qy
AGATAGTTGGGGTGGTAGCCCTGTGCCCCATGATGAAACATACTGTGACCC	AAGCGAG	1480	Db
lulleValGlyValValGluProValProHisAspGluThrTyrCysAsp	ArgG	481	Qy
GTCTTTAAAGGGGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGAT	TGGATGG	1420	Db
ValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpG	rpMetV	461	Qy
GCACTCACGATTGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAG	AAACAAG	1360	Db
AlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrp	· <u></u>	441	Qy
	65	1300	Db
LeuLeuSerProAspPheGlnGluAspAsnGluThrGluIleAsnPheLeu	eG1	421	Qy

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FITLE OF INVENTION: Human Gene Polynucleotides, Polynucle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09969384 Publication No. US20020192749A1 GENERAL INFORMATION:
APPLICANT: Moore, et al.
                                                                                                                                                                                                                      NAME/KEY: SITE
LOCATION: (2702)
OTHER INFORMATION: n
                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2920
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                  NAME/KEY: SITE LOCATION: (2757) OTHER INFORMATION:
                                         NAME/KEY: SITE
LOCATION: (278)
                                                                                                                                                      LOCATION: (2749)
OTHER INFORMATION:
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LOCATION: (1707)
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LOCATION: (2835)
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LOCATION: (2819)
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                                           aTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGlyCysLe 262
                                                                                                                                                              rTrpArgGlyAspTyrGluValAsnGlyValAspGlyTyrAspTyrSerArgGlyGlnLe 222
                                                                                                                                                                                                                                                          uTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGlyAspTy
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      pAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeuProAs

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      GGATGCACAGAGATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTTGGTCTTCCTAA

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                        gGluIleValGlyValValGluProValProHisAspGluThrTyrCysAspProAlaSe 502
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rPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysValArgIl
                                                                                     sserGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsnValAr 582
                                                                                                                                      saspIleSerAsnSerThrGluAlaGlyGlnLysLeuPheAsnMetLeuArgLeuGlyLy
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                                                                          ATCAGAACCCTGGACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAATGTAAG
                                                                                                                           TGACATCTCAAACTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGNTTGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Applica publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver.
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/969,384
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: PCT/US01/10542
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/236,384
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/194,118
PRIOR FILING DATE: 2000-04-03
                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies FILE REFERENCE: PT055P1
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Moore, et al.
                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                      OTHER INFORMATION:
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LOCATION: (284)
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                                 aTyrValArgAlaLysLeuMetAsnAlaTyrProSerTyrIleSerProIleGlYCysLe
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|CTATGTGAGGCCAAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGATGCCT
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CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/133,952
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/151,181
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 09/563,516
PRIOR FILING DATE: 2000-05-03
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LENGTH: 2638
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APPLICANT: Petrie, Charles
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
FILE REFERENCE: 99-24C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ
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APPLICANT: Piddington, Christopher S.
APPLICANT: Petrie, Charles
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
FILE REFERENCE: 99-24C1
CURRENT APPLICATION NUMBER: US/09/978,385
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/133,952
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/151,181
PRIOR APPLICATION NUMBER: 60/55,181
PRIOR APPLICATION NUMBER: 09/563,516
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-3
PRIOR FILING DATE: 1999-08-3
PRIOR FILING DATE: 1999-08-3
PRIOR FILING DATE: 1999-08-7

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                                  TyrGlnPheGlnPheGlnGluAlaLeuCysGlnAlaAlaLysHisGluGlyProLeuHis
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                                                                             APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: ZACEZ: A HUMAN METALLOENZYME
FILE REFERENCE: 99-24C1
CURRENT APPLICATION NUMBER: US/09/978,385
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/133,952 PRIOR FILING DATE: 1999-05-13 PRIOR APPLICATION NUMBER: 60/151,181 PRIOR FILING DATE: 1999-08-27 PRIOR APPLICATION NUMBER: 09/563,516
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APPLICANT:
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Shoemaker, Kimberly E.
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; LOCATION: (1)...(2415)
; LOCHER INFORMATION: n = A,T,C
US-09-978-385-3
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                                              GluGluTyrValValLeuLysAsnGluMetAlaArgAlaAsnHisTyrGluAspTyrGly
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                              GTNMGNCCNYTNYTNAAYTAYTTYGARCCNYTNTTYACNTGGYTNAARGAYCARAAYAAR
                                                  ValArgProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysAspGlnAsnLys 600
                                                                                          GGNAARWSNGARCCNTGGACNYTNGCNYTNGARAAYGTNGTNGGNGCNAARAAYATGAAY 1740
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; OTHER INFORMATION: n = A,T,C US-09-978-385-7

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Patent No. US20020177211A1
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                                                                                                                                                                       SEQ ID NO 7
                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/978,385
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION ON MADER: 60/133,952
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/151,181
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 09/563,516
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Piddington, Christopher S.
APPLICANT: Petrile, Charles
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
FILE REFERENCE: 99-24C1
                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/151/181
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 09/563,516
PRIOR FILING DATE: 2000-05-03
                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 11 SOFTWARE: FastSEQ for Windows Version
                                                                                             LENGTH: 2415
TYPE: DNA
ORGANISM: Artificial Sequence
NAME/KEY: misc_feature LOCATION: (1)...(2415)
                                         OTHER INFORMATION: This degenerate sequence encodes the amino OTHER INFORMATION: sequence of SEQ ID NO:6.
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YTNACNGTNCCNTTYGCNCARAARCCNAAYATHGAYGTNACNGAYGCNATGATGAAYCAR
                    LeuThrValProPheGlyGlnLysProAsnIleAspValThrAspAlaMetValAspGln
                                                                                                     CysLeuProAlaHisLeuLeuGlyAspMetTrpGlyArgPheTrpThrAsnLeuTyrSer
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1980	YMGNWSNWSNGTNGCNTAYGCNATGMGNAARTAYTTYWSNATHATHAARAAY	1921
6	yrLeuPheArgSerSerValAlaTyrAlaMetArgGlnTyrPheLeuLysValLysAsn	641
640 1920	ArgileSerLeuLysSerAlaLeuGlyAspLysAlaTyrGluTrpAsnAspAsnGluMet (621 1861
620 1860	AsnSerPheValGlyTrpSerThrAspTrpSerProTyrAlaAspGlnSerIleLysVal (
1800	ValargProLeuLeuAsnTyrPheGluProLeuPheThrTrpLeuLysaspGlnasnLys	581 1741
580 1740	ysSerGluProTrpThrLeuAlaLeuGluAsnValValGlyAlaLysAsnMetAsn 	
560 1680	LysCysAspIleSerAsnSerThrGluAlaGlyGlnLysLeuDheAsnMetLeuArgLeu 	
540 1620	euHis TNCAY	0 N
520 1560	AlaSerLeuPheHisValSerAsnAspTyrSerPheIleArgTyrTyrThrArgThrLeu 	501 1501
500 1500	alProHisaspGluThrTyrCysaspPro rnCCNCayGaYGARACNTAYTGYGAYCCN	481 1441
480 1440	TrpMetValPheLysGlyGluIleProLysAspGlnTrpMetLysLysTrpTrpGluMet	461 1381
460 1380	LysGlnAlaLeuThrIleValGlyThrLeuProPheThrTyrMetLeuGluLysTrpArg	441 1321
440 1320	IleGlyLeuLeuSerProAspPheGlnGluAspAsnGluThrGluTleAsnPheLeuLeu 	421 1261
420 1260	HisGlualaValGlyGluIleMetSerLeuSerAlaAlaThrProLysHisLeuLysSer 	1201
400 1200	TyraspmetalaTyralaalaGlnProPheLeuLeuArgasnGlyAlaasnGluGlyPhe	381 1141
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360 1080	LysalaValCysHisProThralaTrpAspLeuGlyLysGlyAspPheArgIleLeuMet	, 341) 1021
340 1020	ProAsnMetThrGlnGlyPheTrpGluAsnSerMetLeuThrAspProGlyAs	, 321) 961
320 960	AlaTrpAspAlaGlnArgIlePheLysGluAlaGluLysPhePheValSerValGlyLeu 	7 301 5 901

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                      801 ValGlnThrSerPhe 805
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                                                          TyrAlaSerIleAspIleSerLysGlyGluAsnAsnProGlyPheGlnAsnThrAspAsp 800
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